

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 00:16:06 ; Search time 467 Seconds
(without alignments)
10599.341 Million cell updates/sec

Title: US-09-913-858a-1

Perfect score: 2198

Sequence: 1 actaactcaacgctgatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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- 4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
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- 22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2198	100.0	2198	21	AAA97937 Mung bean alpha 1,
2	661.6	30.1	1982	21	AAC39529 Arabidopsis thalia
3	209.4	9.5	2069	22	AAF84907 Nitrogen-inducible
4	209.4	9.5	2124	22	AAF84910 Nitrogen-inducible
5	209.4	9.5	2165	22	AAF84913 Nitrogen-inducible
6	209.4	9.5	2232	22	AAF84916 Nitrogen-inducible
7	209.4	9.5	2808	22	AAF84906 Nitrogen-inducible
8	209.4	9.5	2863	22	AAF84909 Nitrogen-inducible
9	209.4	9.5	2904	22	AAF84912 Nitrogen-inducible

10	209.4	9.5	2971	22	AAF84915 Nitrogen-inducible
11	209.4	9.5	3714	22	RAF84905 Nitrogen-inducible
12	209.4	9.5	3775	24	AD38881 Alfalfa AP2 adapto
13	105	4.8	105	21	AA97938 Mung bean alpha 1,
14	84.2	3.8	287	24	ABL78406 Corn tassels-derive
15	50	2.3	1461	21	AA40119 Arabidopsis thalia
16	49.2	2.2	676	22	AA541344 cDNA encoding nove
17	49.2	2.2	1328	24	ABK11711 Human fucosyltrans
18	49.2	2.2	1479	24	ABA05334 Human fucosyltrans
19	49.2	2.2	2557	24	ABA05333 Human fucosyltrans
20	47.6	2.2	398	22	AAF64428 Novel human polynu
21	47	2.1	34769	22	AA546775 Tumour suppressor
22	46.6	2.1	34769	22	AA546775 Tumour suppressor
23	46	2.1	5931	22	AA546703 Human chemically p
24	45.8	2.1	6136	24	ABK40042 Human cervical can
25	45	2.0	612	22	AAH71471 Signal transductio
26	44.8	2.0	9814	24	ABK31429 Human immune syste
27	44.2	2.0	10020	24	ABL34293 Chemically pretrea
28	44.2	2.0	12405	22	AA545330 Human gene regulat
29	44.2	2.0	12405	24	AA561143 DNA transcription
30	44.2	2.0	12405	24	ABK28169 Human prostate exp
31	43.6	2.0	626	23	ABV60941 Murine alpha-1,3-f
32	43.6	2.0	2036	21	AAZ92672 Murine immune syste
33	43.6	2.0	2170	21	AAZ92645 Chemically pretrea
34	43.6	2.0	113515	24	ABL34175 Human alpha-1,3-fu
35	43.4	2.0	5857	24	AA563347 Human immune syste
36	43.2	2.0	2676	21	AAZ92647 Human alpha-1,3-fu
37	43.2	2.0	2822	21	AAZ92646 Human immune syste
38	43	2.0	10377	24	ABL34221 Human immune syste
39	42.6	1.9	9652	24	ABL32908 Arabidopsis thalia
40	42.4	1.9	1465	21	AAC40055 Arabidopsis thalia
41	42.4	1.9	1563	21	AAC41754 Arabidopsis thalia
42	42.2	1.9	626	23	ABV60941 Human prostate exp
43	41	1.9	1373	21	AAZ77739 Lung cancer associ
44	41	1.9	4063	21	AAF18226 Human immune syste
45	41	1.9	5593	24	ABL33161

ALIGNMENTS

RESULT 1

AAA97937

ID AAA97937 standard; DNA; 2198 BP.

XX AAA97937;

AC AAA97937;

DT 26-JAN-2001 (first entry)

XX 1

DE Mung bean alpha 1,3-fucosyltransferase DNA.

XX alpha 1,3-fucosyltransferase; plant; mung bean; glycoprotein; insect;

XX G1cNac-alpha1,3-fucosyl transferase; ds.

XX Phaseolus aureus.

XX WO200049153-A1.

XX 24-AUG-2000.

XX 17-FEB-2000; 2000WO-AT00040.

XX 18-FEB-1999; 99AT-0000270.

XX (ALTM/ ALT) ALTMAN F.

XX Altman F;

XX WPI; 2000-549274/50.

XX P-PSDB; AAB10713.

XX DNA encoding plant G1cNac-alpha-1,3-fucosyl transferase, useful for

XX recombinant production of the enzyme and recombinant glycoprotein

PT

RESULT 2

```

US-09-878-574-7836
: Sequence 7836 Application US/09878574
: Patent No. US20070110548A1
: GENERAL INFORMATION:
: APPLICANT: Byrum, Joseph R.
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Thompson, Michael D.
: TITLE OF INVENTION: Nucleic Acid Molecules
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(13401)B
: CURRENT APPLICATION NUMBER: US/09/878,574
: PRIOR FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 09/333,535
: PRIOR FILING DATE: 1999-06-14
: NUMBER OF SEQ ID NOS: 1575
: SEQ ID NO 7836
: LENGTH: 273
: TYPE: DNA
: ORGANISM: Glycine max
: OTHER INFORMATION: Clone ID: 701100402H1
US-09-878-574-7836

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Query Match	3.8%	Score 83.4;	DB 10;	Length 273;
Best Local Similarity	79.4%;	Prod. No. 2.5e-13;		
Matches 112;	Conservative	0;	Mismatches 26;	Indels 3; Gaps 1;
984	CCGTGATGGAGAGCTGAACAAGCTGGAGCCCTGGAAGCACTACAAATTTAGCTTAGCCTT	1043		
1	CCGTGATGGAGAGCTGGACAAGCTGGAGCCCTGGAAGCACTACAAATTTAGCTTAGCATT	60		
1044	TGAANAATTCGAATCAGGAAGATATGTAACTGAGAAAAT---TCTTCCAATCCCTTTGTGC	1100		
61	TGAGAAATCTAGCGATGTAGATTAACTAACTTGAATGCTCTGTACAAATGCCATTGTTAC	120		
1101	TGGAACATGCTCCCTGTGGTTGT	1121		
121	TGGATCTTAAAGGTGTGGGTGT	141		
Db				

RESULT 3

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US-09/918-995-2051
: Sequence 2051, Application US/09918995
: Publication No. US20030073623A1
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCING METHOD
: FILE REFERENCE: 20411-756
: CURRENT APPLICATION NUMBER: US/09/918,995
: CURRENT FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: US/09/235,076
: PRIOR FILING DATE: 1999-01-20
: NUMBER OF SEQ ID NOS: 38054
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2051
: LENGTH: 477
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(477)
: OTHER INFORMATION: n = A,T,C or G
US-09/918-995-2051

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	Query Match	2.2a	Score 49.2	DB 9	Length 477
	Best Local Similarity	49.2a	Prod. NO. 0.0017		
	Matches 129	Conservative	0	Mismatches 133	Indels 0 Gaps 0
100y	1007	TGGAAGCCCTGAGACACTACAAATTTAGCTTTAGCTTTGAAATTCGAATGAGGAAGATT	1066		
0b	75	TGGCTTTCTTCTCCCGCTATTAAGTTCACCTTGCCCTCGAAANTGCCATCTGTACGACT	134		

[illegible]

RESULT 4

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US-09-960-352-12673/C
: Sequence 12673, Application US/09960352
: Patent No. US20020137139A1
: GENERAL INFORMATION:
: APPLICANT: Warren, Wesley C.
: APPLICANT: Tao, Mengbing
: APPLICANT: Byatt, John C.
: APPLICANT: Mathialagan, Nagappan
: TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
: TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
: FILE REFERENCE: 16511.006/37-21(10298)C
: CURRENT APPLICATION NUMBER: US/09/960.352
: CURRENT FILING DATE: 2001-09-24
: NUMBER OF SEQ ID NOS: 15112
: SEQ ID NO 12673
: LENGTH: 277
: TYPE: DNA
: ORGANISM: Bos taurus
: OTHER INFORMATION: Clone ID: 54-LIB3058-039-01-K1-F10
US-09-960-352-12673

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Query Match	1.98;	Score 41.2;	DB 10;	Length 277;
Best Local Similarity	55.6%;	Pred. No. 0.21;		
Matches	79;	Conservative 0;	Mismatches 63;	Indels 0; Gaps 0;
QY	2057	TTACTTCATGTGTTTTCATCATCTCCAGACCTTTT	TAGTCTCGGAAC	TGTCCTCGTGGT 2116
Db	258	TTTTTTTTTTTTTATTTTTTTTTTTTTTTTTTTTT	TATATTTCCAAAA	TTTTTTTCATTTT 199
QY	2117	TTGAGCACCTGTTATTCCTTCAGTGTTACTGTCC	AGTGGTATTCGTTT	TGACCTCTAA 2176
Db	198	TTAAAAATTTTTTCTTTTTTAAATTTTTTAA	TAAATTTTTTTTTT	TTTTTTTTTAAAAA 139
QY	2177	AAAAAAAAAAAAAAAAAAAAAAAAA	AAAAA	2198
Db	138	AAAAAAAAAAAAAAAAAAAAAAAAA	AAAAA	117

085117

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: RESULT 5
: US-09-925-301-133
: Sequence 133, Application US/09925301
: Patent No. US20020052308A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA106
: CURRENT APPLICATION NUMBER: US/09/925,301
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05882
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1694
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 133

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production -
Claim 1: Page 35-36; 72pp: German.
This invention describes a novel DNA molecule (I), encoding a plant protein with fucosyl transferase activity, GlcNAc-alpha1,3-fucosyl transferase. The methods and DNA sequences are useful for production of recombinant GlcNAc-alpha1,3-fucosyltransferase. The enzyme is useful for the production of recombinant human glycoproteins, which are especially useful in medical applications and pharmaceutical compositions. (I) can be used as a probe to select GlcNAc-alpha1,3-fucosyltransferase coding sequences in a sample, especially from plants or insects. This sequence encodes the mung bean (*Phaseolus aureus*) alpha 1,3-fucosyltransferase protein described in the method of the invention.

Sequence 2198 BP; 595 A; 412 C; 518 G; 673 T; 0 other;

Query Match 100.0%; Score 2198; DB 21; Length 2198;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACTAACTCAACGCTGATTTCTTTTCTTTTCAGGAAACCATCCACCCATAACACAA 60
DB 1 ACTAACTCAACGCTGATTTCTTTTCTTTTCAGGAAACCATCCACCCATAACACAA 60
OY 61 AAAAACAACAGCAGCTGTGTTTTTATCGTCTTTTCTTTTAAACAAGCACCCCA 120
DB 61 AAAAACAACAGCAGCTGTGTTTTTATCGTCTTTTCTTTTAAACAAGCACCCCA 120
OY 121 TCATGGAATCGTCTCATAACGCCAAATTTTCCATTTCCCTTTGATTTTATTTT 180
DB 121 TCATGGAATCGTCTCATAACGCCAAATTTTCCATTTCCCTTTGATTTTATTTT 180
OY 181 TCGGAAATTCGCAAGTTGGGGGCCAATGAATGATGGCTGTGTGACGAATCTTCGAGGC 240
DB 181 TCGGAAATTCGCAAGTTGGGGGCCAATGAATGATGGCTGTGTGACGAATCTTCGAGGC 240
OY 241 TCGAGACAGATGGGCCAACAGACGTTACCCGTTTGGCTTCGGGAGGCAACCCA 300
DB 241 TCGAGACAGATGGGCCAACAGACGTTACCCGTTTGGCTTCGGGAGGCAACCCA 300
OY 301 AAGAGGAATGGAGCAATTAATGCTCTTTGTTGGCCCTTTGTTGGTATCGCGGAGATC 360
DB 301 AAGAGGAATGGAGCAATTAATGCTCTTTGTTGGCCCTTTGTTGGTATCGCGGAGATC 360
OY 361 CGGTTTCTGGGTAGTTGGATATGGCCAAACGCCCATGGTTGACTCCCTCGCTGAC 420
DB 361 CGGTTTCTGGGTAGTTGGATATGGCCAAACGCCCATGGTTGACTCCCTCGCTGAC 420
OY 421 TTCTTCTACCGCTCTGAGCGGTCTGTTGAAGTGAAGATTTGGGGTTGGGTTGGTGGCT 480
DB 421 TTCTTCTACCGCTCTGAGCGGTCTGTTGAAGTGAAGATTTGGGGTTGGGTTGGTGGCT 480
OY 481 TCTGATCGGAATCTGAATCGTATAGTTGTGAGGAATGTTGGAGAGGAGGATGCTGTC 540
DB 481 TCTGATCGGAATCTGAATCGTATAGTTGTGAGGAATGTTGGAGAGGAGGATGCTGTC 540
OY 541 ACGTATTCGAGGGGCTTTTCCAAAGAGCTATTTTGTGTTCTGGAGCTGATCAGAGTGG 600
DB 541 ACGTATTCGAGGGGCTTTTCCAAAGAGCTATTTTGTGTTCTGGAGCTGATCAGAGTGG 600
OY 601 AAGTCGTGTTGGTGGATGAATTTGGGTTTACTGGGGATGAAGAGCCAGATGCCCA 660
DB 601 AAGTCGTGTTGGTGGATGAATTTGGGTTTACTGGGGATGAAGAGCCAGATGCCCA 660
OY 661 TTTGGGTTTACCTCAACCAAGTGGACAGCTAGCATTCCTGCGGATCAATGGGAATCAGCAGAA 720
DB 661 TTTGGGTTTACCTCAACCAAGTGGACAGCTAGCATTCCTGCGGATCAATGGGAATCAGCAGAA 720
OY 721 TACTATCTGAGAACAAATATTGCCATGGCAAGACGGGGGATATACATCGTAATGACA 780
DB 721 TACTATCTGAGAACAAATATTGCCATGGCAAGACGGGGGATATACATCGTAATGACA 780

OY 781 ACCAGTCTATCTTCGGATGTTCTCTGTTGGATATTTTTTTCATGGCTGAGTATCATATGATG 840
DB 781 ACCAGTCTATCTTCGGATGTTCTCTGTTGGATATTTTTTTCATGGCTGAGTATCATATGATG 840
OY 841 GCACAGTGCAGCGCAAAACCTGAAGCTGCTTCTGCAGCTGCTTTTCCAAATTTCTGCT 900
DB 841 GCACAGTGCAGCGCAAAACCTGAAGCTGCTTCTGCAGCTGCTTTTCCAAATTTCTGCT 900
OY 901 GCTCGAAATTTCCGTTGCAAGCTCTTGAAGCCCTTGAAGAAATCAACATCAAAATTTCT 960
DB 901 GCTCGAAATTTCCGTTGCAAGCTCTTGAAGCCCTTGAAGAAATCAACATCAAAATTTCT 960
OY 961 TCTATGTTGTTGTCACAGAACCCGTCATGGAAGAGTGAACAAAGTGAAGCCCTGAAG 1020
DB 961 TCTATGTTGTTGTCACAGAACCCGTCATGGAAGAGTGAACAAAGTGAAGCCCTGAAG 1020
OY 1021 CACTACAAATTTAGCTTAGGCTTTGAAATTTTGAATGAGGAAGATTTGTAACCTGAAAA 1080
DB 1021 CACTACAAATTTAGCTTAGGCTTTGAAATTTTGAATGAGGAAGATTTGTAACCTGAAAA 1080
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DB 1081 TTCTTCCAAATCCCTGTTGCTGGAACCTGCTGCTGCTGTTGTTGCTGCTCAAAATTTCT 1140
OY 1141 GACTTTGCTCTCTCTCTCTGTTTACATATTTAAAGAGATAGAGATGTTGAGTCT 1200
DB 1141 GACTTTGCTCTCTCTCTCTGTTTACATATTTAAAGAGATAGAGATGTTGAGTCT 1200
OY 1201 GTTCAAGACCATGAGATATCTAGCAGAAATCCCGAAGCATATATCAATCATTTGAGG 1260
DB 1201 GTTCAAGACCATGAGATATCTAGCAGAAATCCCGAAGCATATATCAATCATTTGAGG 1260
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DB 1261 TGGAGATGATGAGGTCTCTGCTGCTCAAGCCCTTGTGATATGCGAGCTGTGCTAT 1320
OY 1321 TCATCTGCTGCTCTCTCTCTGCTTGCACATTTGAGTGTAGAGAGAAAGAAATTAAT 1380
DB 1321 TCATCTGCTGCTCTCTCTCTGCTTGCACATTTGAGTGTAGAGAGAAAGAAATTAAT 1380
OY 1381 CCAAGCTTAAAGACACGCTCTTGCACATTTGAGTGTAGAGAGAAAGAAATTAAT 1440
DB 1381 CCAAGCTTAAAGACACGCTCTTGCACATTTGAGTGTAGAGAGAAAGAAATTAAT 1440
OY 1441 TATGTCAGAGAAAGGGAAGGTTGAGATGGAGTCCATTTACCTGAGTCTAGCAATTTA 1500
DB 1441 TATGTCAGAGAAAGGGAAGGTTGAGATGGAGTCCATTTACCTGAGTCTAGCAATTTA 1500
OY 1501 ACTCTGAATGCTGGAAGGCTGCTGTTGTTTGAAGTTCACATCCCTGAATCTTGTGCT 1560
DB 1501 ACTCTGAATGCTGGAAGGCTGCTGTTGTTTGAAGTTCACATCCCTGAATCTTGTGCT 1560
OY 1561 GTATGGAAGACTGAAGGCTGGAAGTTATGAAGGGGGAGTGTGTTTAAACTCTACAAA 1620
DB 1561 GTATGGAAGACTGAAGGCTGGAAGTTATGAAGGGGGAGTGTGTTTAAACTCTACAAA 1620
OY 1621 ATATACCAATTTGCTGTGACACAGACAGCTCTTTATACCTTCAGCTTCAAGAGTGTAT 1680
DB 1621 ATATACCAATTTGCTGTGACACAGACAGCTCTTTATACCTTCAGCTTCAAGAGTGTAT 1680
OY 1681 GCTGATTTACGAGTCTGCTTTGGAGAAACATCTCTGTCACAGTGTGAAAGTCAATTTTGTG 1740
DB 1681 GCTGATTTACGAGTCTGCTTTGGAGAAACATCTCTGTCACAGTGTGAAAGTCAATTTTGTG 1740
OY 1741 TAGCATCGCTAAATGCTGCTGCTACCTGATAGTCTTACCTAGCTAGTACACTA 1800
DB 1741 TAGCATCGCTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
OY 1801 GCTAGAGTTTATGAGATGAGTATGCGAGTGAATATGGCATGCTTTTATTTATGCTAGT 1860
DB 1801 GCTAGAGTTTATGAGATGAGTATGCGAGTGAATATGGCATGCTTTTATTTATGCTAGT 1860
OY 1861 TCTTGGCCAACTCATTTGATGTTTGTATGAAGACATCACACTTTTAACTTTGTTTC 1920

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Db 1861 TCTGGCCAACTCATTTGATGTTTGTATGAAGACATCACACTTTAATTTAAACTGTTTC 1920
Oy 1921 TGTAGAAGTCAATCATATTAATGCTTACTGTTTACTGCTTACTGATCATCTAGA 1980
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Oy 1981 AGTCACAGTCTTGTATATGTTGAGTGAAGAACTGAAATCTAATAGAAGGATCAGATGTTT 2040
Db 1981 AGTCACAGTCTTGTATATGTTGAGTGAAGAACTGAAATCTAATAGAAGGATCAGATGTTT 2040
Oy 2041 CACTCAAGACACATTAATTTACTTCTGTTGTTGATGATCTCGAGCTTTTACTGTCG 2100
Db 2041 CACTCAAGACACATTAATTTACTTCTGTTGTTGATGATCTCGAGCTTTTACTGTCG 2100
Oy 2101 GAACCTCCCTGGTGTTCAGCACCTGTTATGCTTCACTGTTTACTGTCAGTGGTTATC 2160
Db 2101 GAACCTCCCTGGTGTTCAGCACCTGTTATGCTTCACTGTTTACTGTCAGTGGTTATC 2160
Oy 2161 GTTTTGAACCTCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2198
Db 2161 GTTTTGAACCTCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2198

RESULT 2
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ID AAC39529 standard; DNA; 1982 BP.
XX
AC AAC39529;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24967.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 03-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0123788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
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PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
```


Db 1155 GCAGTTGCAAGAGAAATGAAGTATCTGCGAGTAACCTGCTCTTATAATCAGACACT 1214
 Qy 1257 GAGGTGGAAGTATGAGGTCCATCTGACTCTCTCAAGGCCCTTGTGATATGCGACTGT 1316
 Db 1215 AAGATGGAATACGAGGCTCTTCAAGTCTTCAAGGCACCTGTTGATATGCTGCTGT 1274
 Qy 1317 GCATTCATGCTGCTCTTCTTGCATTCACCTGGCCACAGTGTAGTAGAGAGAAAGAAA 1376
 Db 1275 ACACCTCTCTTCTGCTCTCTGATTTCTGCTGCGCCACGAGGTGCGAAGCAAGAGAGGA 1334
 Qy 1377 TAATCAAGCCTTAAGAGACGCTCTTGAAGT---GCACTAGAGGGCCAGAAACCGTATA 1433
 Db 1335 AAGCCCTAATTTCAAGAAACGACCTGCAATGTAGCAGGGGAGGATCAGACACACTTTA 1394
 Qy 1434 TCATATCTATGTCAGAGAAAGGGAGGTTTGAGATGGAGTCCATTTACCTGAGGCTAG 1493
 Db 1395 TCATGTTTGTGTAGAGAAAGAGCGCGTGTGAAATGGAATCAGTCTTTTGTAGGGGTAA 1454
 Qy 1494 CAATTTAAGTCTGAATGCTGAAGGCTGCTGTTGTTTGAAGTTCACATCCCTGAATCT 1553
 Db 1455 AAGTGTGACTCAGGAAGCTCTAGATCTGCAATCTGCAATCTGCGCAAGTTCAGTCTTTAAACA 1514
 Qy 1554 TGTGCTGTATGGAAGTCTGAAGGCTGGAAGTATTAAGAGGGGGAGTCTTTAAACT 1613
 Db 1515 TGAGGCACTGTCAGAGAAAGGAGGCTGGAACCTTAAGGAGACAAAGAGCTTAAAT 1574
 Qy 1614 CTACAAATATACCCANTTGGCTTGACACAGAGACAGCTCTTTATACCTTCAGCTTCAA 1673
 Db 1575 ACATGGATTTACCGCTTGGCTTAACGCAACGACAGCGCTTTGACAACTTCAAAATTCGA 1634
 Qy 1674 AGTGTATGCTGATTTTCAGAGTCTACTTGGAGAACAACTCTTGTGCCAAGTGTGAAGTCTAT 1733
 Db 1635 GCGAAATTCGAGTCTAAGTAGTACATTCACATTCAAACAAACCTTGTGCTAAATTTGAGGTTGT 1694
 Qy 1734 TTTTGTGTAG 1743
 Db 1695 CTTCGCTAG 1704

RESULT 3

AAF84907
 ID AAF84907 standard; DNA; 2069 BP.

AC AAF84907;

XX 09-JUL-2001 (first entry)

DE Nitrogen-inducible promoter for regulating foreign gene expression.

XX nitrogen-inducible promoter; nitrite reductase gene; NIR gene;

KW transgenic plant; transgene expression; ss.

XX Synthetic.

OS

XX WO200125454-A2.

PN

XX 12-APR-2001.

PD

XX 02-OCT-2000; 2000WO-C01143.

PF

XX 04-OCT-1999; 99US-0157133.

PR

XX (MEDI-) MEDICAGO INC.

PA

XX Vezina L, D'Aoust M;

PI

XX WPI; 2001-308228/32.

DR

XX Regulating foreign gene transcription in transgenic plants, comprises

PT transforming a plant (cell) with an expression construct having

PT nitrogen-inducible promoter, an open reading frame of a gene and a

PT polyadenylation site

xx Claim 1; Page 30-31; 44pp; English.
 PS

CC AAF84905-17 represent nitrogen-inducible promoters. They are promoters
 CC of the nitrite reductase (NIR) gene. The promoter is used for regulating
 CC foreign gene transcription in transgenic organisms. The method uses an
 CC expression construct having a nitrogen-inducible promoter, with(out)
 CC cis-acting sequence, operably linked to the gene to be expressed and
 CC modulated for transcriptional expression of the gene by addition or
 CC removal of a nitrogen inducer, an open reading frame of a gene, and a
 CC 3' polyadenylation signal. The method is useful for regulating the
 CC transcription of transgenes in genetically modified organisms. The
 CC nitrogen-inducible expression cassettes are useful for the controlling
 CC expression of foreign genes in plants.
 XX

SQ Sequence 2069 BP; 640 A; 389 C; 335 G; 705 T; 0 other;

Query Match 9.5%; Score 209.4; DB 22; Length 2069;

Best Local Similarity 66.5%; Pred. No. 2.5e-45;

Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

Qy 1486 AGGCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTTGAAGTTCACATCC 1545

Db 170 AGATCTAGCAATTTAACTCTGAGTCTCTCAAGCTGCTGTTTACGAAGTTCACGTC 229

Qy 1546 CTGAATCTGCTGCTGATGGAAGACTGAAAGCCCTGAAGTTTAAAGAGGGGGAGTGT 1605

Db 230 CTGAATCATGCTGCTGATGGAAGCCCTGAAGACCTCAAAATTTCTAAAGGTGGCGATAA 289

Qy 1606 TTAAGCTCTACAAATATATACCAATTTGGCTTGACACAGACAGCAAGCTCTTTATACCTTC 1665

Db 290 TTGAAGGTTTACAAATATATACCTCTGCGGGCTTGACACAGAGGCAAGCTCTTTATACCTTC 349

Qy 1666 AGCTTCAAGGAGTGTGCTGATTTTCAGGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 1725

Db 350 CAGTTCAAGCGGGGATGTTGATTTTCAGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 409

Qy 1726 GAAGTCAATTTTGTGAGCATGCGCTAA-----ATGCTACCTCTGCTCTACCTGAAT 1778

Db 410 GAAGTCAATTTTGTGAGCATATGTTGAGCTACCTACCTACAAATTTACATGATCATACCTAGCAAT 469

Qy 1779 AGCTTCACTTAGCTGAGCATAGTATGAGTGTGAGCAATGAGTGGCAGTGAATATGCG 1838

Db 470 AGCTCTTCACTTAACCTGACAGAAATGAAGTTTATGGAATGAGTATGACCATGGAGTCGCGC 529

Qy 1839 ATGGCTT-----TATTTATGCTAGTCTTCTTGGCCAACTCATTTGATGTTT 1884

Db 530 ATGGCTTGTAAAGCTTACCTACTTTGGCCAACTCATCGGGGATTTACATTCAGAAAT 589

Qy 1885 GTATAAGACATCAGACTTTAAATTTTAACTTGTGTTCTGTAGAAGTGCAATCCATATTTA 1944

Db 590 ATACATGACTTCAACCACTACTTAAACCCCTTTTGTGAAGATAACTGAATGTTTCATATTTA 649

Qy 1945 ATGCTTAGTGTAGTGTCTTATCTGATCATCT 1977

Db 650 ATGTTGGGTTGTAGTGTGTTTACTTGATATAT 682

RESULT 4

AAF84910

ID AAF84910 standard; DNA; 2124 BP.

XX

AC AAF84910;

XX

XX 09-JUL-2001 (first entry)

DT

XX Nitrogen-inducible promoter for regulating foreign gene expression.

DE

XX nitrogen-inducible promoter; nitrite reductase gene; NIR gene;

KW transgenic plant; transgene expression; ss.

XX

OS Synthetic.

XX

PN WO200125454-A2.
XX 12-APR-2001.
XX 02-OCT-2000; 2000WO-CA011143.
XX 04-OCT-1999; 99US-0157133.
XX (MEDI-) MEDICAGO INC.
XX Vezina L, D'Aoust M;
XX WPI; 2001-308228/32.
XX
XX Regulating foreign gene transcription in transgenic plants, comprises
XX transforming a plant (cell) with an expression construct having
XX nitrogen-inducible promoter, an open reading frame of a gene and a
XX polyadenylation site
XX
XX Claim 1: Page 32-33; 44pp: English.
XX
XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters
XX of the nitrite reductase (NIR) gene. The promoter is used for regulating
XX foreign gene transcription in transgenic organisms. The method uses an
XX expression construct having a nitrogen-inducible promoter, with(out)
XX cis-acting sequences, operably linked to the gene to be expressed and
XX modulated for transcriptional expression of the gene by addition or
XX removal of a nitrogen inducer, an open reading frame of a gene, and a
XX 3' polyadenylation signal. The method is useful for regulating the
XX transcription of transgenes in genetically modified organisms. The
XX nitrogen-inducible expression cassettes are useful for the controlling
XX expression of foreign genes in plants.
XX
XX Sequence 2124 BP: 651 A; 412 C; 339 G; 722 T; 0 other;
XX
XX Query Match 9.5%; Score 209.4; DB 22; Length 2124;
XX Best Local Similarity 66.5%; Pred. No. 2.5e-45;
XX Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;
XX
QY 1486 AGGCTAGCAATTTAACTCTGAATGCTGGAAGGCTGCTGTTGTTTGAAGTTCACATCC 1545
DB 170 AGATCTAGCAATTTAACTCTGGAGTCTCTCAAGACTGCTGTTTACGAAGTTCACGTC 229
QY 1546 CTGAATCTTGCTGCTGATGGAAGACTGAAAGGCTGGAAGTATAGAGGGGGAGTCT 1605
DB 230 CTGAATCATGTTCTGATGGAAGCTGAAAGACCTCAAAATCTTAAAGGTGGCGATAA 289
QY 1606 TTAAACTCTACAAATATACCAATTCGCTTCACACAGACAGACTCTTTATACCTTC 1665
DB 290 TTGAAGGTTTACAAATATACCTCGCGGCTTGACACAGAGGCAAGCTTTTATACCTTC 349
QY 1666 AGCTTAAAGGTGATGCTGATTTGAGGAGTCACTTGGAGAACAAATCTTGTGCCAAGTTT 1725
DB 350 CAGTTTCAACGGGATGTTGATTTTGAAGTCACTTGGAGAACAAATCTTGTGCCAAGTTT 409
QY 1726 GAAGTCAATTTTGTAGCATGCGCTAA-----ATGCTACCTCTGCTACCTGAAT 1778
DB 410 GAAGTCAATTTTGTAGCATGCTGCTGCTACCTACCTACCTAGCAT 469
QY 1779 AGCTTCAATTTAGTGAGCAGTATGATTTAGGATGAGTATGCGAGTGAATATGCG 1838
DB 470 AGCTTCTTCACTTAAGTGAAGTATGATTTAGGATGAGTATGCGAGTGGAGTCGCG 529
QY 1839 ATGCGTT-----TATTATGCTAGTCTTCTTGCCCACTCATTTGATGTTT 1884
DB 530 ATGCGTTTGAATGCTTACCTACTTTTGGCCAACTCATCGGGGATTTACATTCAGAAAT 589
QY 1885 GTATACACATCACTTTAAATTTTAACTTCTTCTGTAGAGTGCATATATTTA 1944
DB 590 ATACATGCTTCAACCACTTAACCCCTTTTGTAGATCAATGAATGTTTATATTTA 649
QY 1945 ATGCTTATGTTTATGCTCTTATCTGATCATCT 1977
DB 1945 ATGCTTATGTTTATGCTCTTATCTGATCATCT 1977

DB 650 ATGTTGGGTTGTAGTGTGTTTACTTGATTATAT 682
XX
XX RESULT 5
XX AAF84913
XX ID AAF84913 standard; DNA; 2165 BP.
XX AC AAF84913;
XX XX
XX DT 09-JUL-2001 (first entry)
XX XX
XX DE Nitrogen-inducible promoter for regulating foreign gene expression.
XX XX
XX KW nitrogen-inducible promoter; nitrite reductase gene; NIR gene;
XX KW transgenic plant; transgene expression; ss.
XX OS Synthetic.
XX XX
XX PN WO200125454-A2.
XX XX
XX PD 12-APR-2001.
XX XX
XX PF 02-OCT-2000; 2000WO-CA011143.
XX XX
XX PR 04-OCT-1999; 99US-0157133.
XX XX
XX PA (MEDI-) MEDICAGO INC.
XX PI Vezina L, D'Aoust M;
XX XX
XX DR WPI; 2001-308228/32.
XX XX
XX PT Regulating foreign gene transcription in transgenic plants, comprises
XX PT transforming a plant (cell) with an expression construct having
XX PT nitrogen-inducible promoter, an open reading frame of a gene and a
XX PT polyadenylation site
XX XX
XX PS Claim 1: Page 35; 44pp: English.
XX XX
XX CC AAF84905-17 represent nitrogen-inducible promoters. They are promoters
XX CC of the nitrite reductase (NIR) gene. The promoter is used for regulating
XX CC foreign gene transcription in transgenic organisms. The method uses an
XX CC expression construct having a nitrogen-inducible promoter, with(out)
XX CC cis-acting sequences, operably linked to the gene to be expressed and
XX CC modulated for transcriptional expression of the gene by addition or
XX CC removal of a nitrogen inducer, an open reading frame of a gene, and a
XX CC 3' polyadenylation signal. The method is useful for regulating the
XX CC transcription of transgenes in genetically modified organisms. The
XX CC nitrogen-inducible expression cassettes are useful for the controlling
XX CC expression of foreign genes in plants.
XX XX
XX SQ Sequence 2165 BP: 664 A; 424 C; 345 G; 732 T; 0 other;
XX
XX Query Match 9.5%; Score 209.4; DB 22; Length 2165;
XX Best Local Similarity 66.5%; Pred. No. 2.6e-45;
XX Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;
XX
QY 1486 AGGCTAGCAATTTAACTCTGAATGCTGGAAGGCTGCTGTTGTTTGAAGTTCACATCC 1545
DB 170 AGATCTAGCAATTTAACTCTGGAGTCTCTCAAGACTGCTGTTTACGAAGTTCACGTC 229
QY 1546 CTGAATCTTGCTGCTGATGGAAGACTGAAAGGCTGGAAGTATAGAGGGGGAGTCT 1605
DB 230 CTGAATCATGTTCTGATGGAAGCTGAAAGACCTCAAAATCTTAAAGGTGGCGATAA 289
QY 1606 TTAAACTCTACAAATATACCAATTCGCTTCACACAGACAGACTCTTTATACCTTC 1665
DB 290 TTGAAGGTTTACAAATATACCTCGCGGCTTGACACAGAGGCAAGCTTTTATACCTTC 349
QY 1666 AGCTTAAAGGTGATGCTGATTTGAGGAGTCACTTGGAGAACAAATCTTGTGCCAAGTTT 1725
DB 350 CAGTTTCAACGGGATGTTGATTTTGAAGTCACTTGGAGAACAAATCTTGTGCCAAGTTT 409

RESULT 9

ID AAF84912 standard; DNA; 2904 BP.

XX AAF84912:

XX 09-JUL-2001 (first entry)

XX Nitrogen-inducible promoter for regulating foreign gene expression.

XX nitrogen-inducible promoter; nitrite reductase gene; NIR gene;

XX transgenic plant; transgene expression; ss.

XX Synthetic.

XX WO200125454-A2.

XX 12-APR-2001.

XX 02-OCT-2000; 2000WO-CA01143.

XX 04-OCT-1999; 99US-0157133.

XX (MEDI-) MEDICAGO INC.

XX Vezina L, D'Aoust M;

XX WPI; 2001-308228/32.

XX Regulating foreign gene transcription in transgenic plants, comprises

XX transforming a plant (cell) with an expression construct having

XX nitrogen-inducible promoter, an open reading frame of a gene and a

XX polyadenylation site

XX Claim 1; Page 34-35; 44pp; English.

XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters
of the nitrite reductase (NIR) gene. The promoter is used for regulating
foreign gene transcription in transgenic organisms. The method uses an
expression construct having a nitrogen-inducible promoter, with(out)
cis-acting sequence, operably linked to the gene to be expressed and
modulated for transcriptional expression of the gene by addition or
removal of a nitrogen inducer, an open reading frame of a gene, and a
3' polyadenylation signal. The method is useful for regulating the
transcription of transgenes in genetically modified organisms. The
nitrogen-inducible expression cassettes are useful for the controlling
expression of foreign genes in plants.

XX Sequence 2904 BP; 903 A; 537 C; 491 G; 973 T; 0 other;

XX Query Match 9.5%; Score 209.4; DB 22; Length 2904;

XX Best Local Similarity 66.5%; Pred. No. 2.9e-45;

XX Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGCTCTAGCAATTAACCTGATGCTGTAAGGCTGCTGTTGTTGAAGTTCAATCC 1545

DB 909 AGATCTAGCAATTAACCTGATGCTGTAAGGCTGCTGTTGTTGAAGTTCAATCC 968

QY 1546 CTGAATCTTGTGCTGTATGGAAGCTGAAAGGCTGAAAGTATAAGAGGGGGAGTGCT 1605

DB 969 CTGAATCTTGTGCTGTATGGAAGCTGAAAGGCTGAAAGTATAAGAGGGGGAGTGCT 1028

QY 1606 TTAAGACTCTACAAATATACCAATTCGCTTGACAGAGACAGCTTTTATACCTTC 1665

DB 1029 TTGAAGTTTACAAATATACCAATTCGCTTGACAGAGACAGCTTTTATACCTTC 1088

QY 1666 AGCTTCAAGGTGATGCTGATTTTACAGAGTCACTTTGGAGACAATCTTGTGCCAAGTTT 1725

DB 1089 CAGTTTCAAGGGGATGTTGATTTACAGAGTCACTTTGGAGACAATCTTGTGCCAAGTTT 1148

QY 1726 GAAGTCAATTTTGTGTAGCATGCGCTAA-----ATGGTACCTCTGCTCACTCAATT 1778

DB 1149 GAAGTAATTTTGTGTAGCATGTTGAGCTACCTACCAATTACATCAGCATT 1208

QY 1779 AGCTTCACTTAGCTGAGCACTAGCTAGCTTTTAGCAATGAGTATGGCAGTAATGGC 1838

DB 1209 AGCTCTTTCACTTAACCTGAGAGAAATGAAGCTTTTAGCAATGAGTATGACCATGGAGTCGC 1268

QY 1839 ATGGCTT-----TATTATGCTAGTTTCTTGCCCAACTCATCTGATGTTT 1884

DB 1369 ATGGCTTTGTAATGCTTACCTACTTTGGCCAACTCATCGGGGATTACATTCAGAAAT 1328

QY 1885 GTATAACACATCACTTAACTTTAACTTCTCTAGCAATGCAATCCATATTA 1944

DB 1329 ATACATGCTTCAACCATACTTAACCCCTTTTGTAGACATAACTGAATGTTCATATTA 1388

QY 1945 ATGCTTAGTTTAGTGTCTTATCTGATCATCT 1977

DB 1389 ATGTTGGTTGTAGTGTCTTTTACTTGATTATAT 1421

RESULT 10

AAF84915

ID AAF84915 standard; DNA; 2971 BP.

XX AAF84915:

XX 09-JUL-2001 (first entry)

XX Nitrogen-inducible promoter for regulating foreign gene expression.

XX nitrogen-inducible promoter; nitrite reductase gene; NIR gene;

XX transgenic plant; transgene expression; ss.

XX Synthetic.

XX WO200125454-A2.

XX 12-APR-2001.

XX 02-OCT-2000; 2000WO-CA01143.

XX 04-OCT-1999; 99US-0157133.

XX (MEDI-) MEDICAGO INC.

XX Vezina L, D'Aoust M;

XX WPI; 2001-308228/32.

XX Regulating foreign gene transcription in transgenic plants, comprises
transforming a plant (cell) with an expression construct having
nitrogen-inducible promoter, an open reading frame of a gene and a
polyadenylation site

XX Claim 1; Page 36-37; 44pp; English.

XX AAF84905-17 represent nitrogen-inducible promoters. They are promoters
of the nitrite reductase (NIR) gene. The promoter is used for regulating
foreign gene transcription in transgenic organisms. The method uses an
expression construct having a nitrogen-inducible promoter, with(out)
cis-acting sequence, operably linked to the gene to be expressed and
modulated for transcriptional expression of the gene by addition or
removal of a nitrogen inducer, an open reading frame of a gene, and a
3' polyadenylation signal. The method is useful for regulating the
transcription of transgenes in genetically modified organisms. The
nitrogen-inducible expression cassettes are useful for the controlling
expression of foreign genes in plants.

XX Sequence 2971 BP; 925 A; 549 C; 508 G; 989 T; 0 other;

XX Query Match 9.5%; Score 209.4; DB 22; Length 2971;

XX Best Local Similarity 66.5%; Pred. No. 3e-45;

XX Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

ID ABL76406 standard; cDNA; 287 BP.
AC ABL76406;
XX
XX
XX 14-MAY-2002 (first entry)
XX
DE Corn tassel-derived polynucleotide (cdps) SEQ ID NO:5780.
XX
XX Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs;
KW inheritance; characteristic; growth; development; disease resistance;
KW environmental adaptability; quality; yield; molecular marker;
KW multigene trait; plant breeding; corn tassel; gene; ss.
XX
XX Zea mays.
XX
XX US2001051335-A1.
XX
XX 13-DEC-2001.
XX
XX 16-APR-1999; 99US-0294093.
XX
XX 21-APR-1998; 98US-082567P.
XX
XX (LALG/) LALGUDI R V.
PA (ITOL/) ITO L Y.
PA (SHER/) SHERMAN B K.
XX
XX Lalgudi RV, Ito LY, Sherman BK;
XX
XX WPT; 2002-163647/21.
XX
XX Novel purified corn tassel-derived polynucleotide useful for
PT determining altered gene expression, to recover regulatory elements and
PT to follow inheritance of desirable characteristics through hybrid
PT breeding programs
XX
PS Claim 1: SEQ ID 5780; 201pp; English.
XX
XX The present sequence describes a purified corn tassel-derived
CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
CC selected from those given in ABL70627 to ABL76833. The cdps sequences
CC encode corn tassel-derived polypeptides (CDPs). The cdps sequences
CC can be used for determining altered gene expression, to recover
CC regulatory elements and to follow inheritance of desirable
CC characteristics through hybrid breeding programs. (I) are also useful
CC in the evaluation, and alteration of desired characteristics associated
CC with growth and development, disease resistance, environmental
CC adaptability, quality and yield, and as molecular markers for studying
CC inheritance of multigene traits, in a plant breeding program. (I) can be
CC used to produce a tassel-specific profile of gene transcription, a
CC transcript image, to clone regulatory elements for use in transformation
CC vectors, to express a polypeptide, to identify, isolate or extend
CC identical or related corn tassel nucleic acid sequences from DNA
CC libraries, in nucleic acid hybridisation or amplification technologies,
CC as query sequences to determine homology of known sequences, as probe
CC for use in Southern or Northern hybridisation, and to identify the
CC presence of and/or to determine the degree of similarity between two
CC (or more) nucleic acid sequences.
XX
XX
XX Sequence 287 BP; 78 A; 57 C; 62 G; 90 T; 0 other;
Query Match 3.8%; Score 84.2; DB 24; Length 287;
Best Local Similarity 67.2%; Pred. NO. 2.5e-12;
Matches 119; Conservative 0; Mismatches 58; Indels 0; Caps 0;
Oy 658 GCATTGGTTACTCAACCAAGTGGACAGTACGATTCCTCGGATCAATGGAATCAGCA 717
Db 39 GGACTGGAGTAATGCTACATCTTCTGTAGAGGGTATCTTCGGATCAATGGAATCATCT 98
Oy 718 GAATACATCTCCTGAGAACAAATATTTGCGATGGCAAGCAGGGGATACATGTAATG 777
Db 99 CAATATTATTCAAGAAATAGTATTGATGCTGCGGCTCGAGGAGGCTACAGATTGTGATG 158

Oy 778 ACAACAGCTATCTTCGGATGTTCCCTGTTGGATATTTTTCATGGCTCAGTATGAT 834
Db 159 ACAATCAGCCTTTCTTCACACGCTCCAGTTGGCTACTCTTTCATGGCTGAATATGAT 215
RESULT 15
AAC40119
ID AAC40119 standard; DNA; 1461 BP.
XX
XX AAC40119;
AC
XX
XX 17-OCT-2000 (first entry)
DT
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 27123.
DE
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 06-APR-1999; 99US-0127462.
PR 08-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
PR 18-APR-1999; 99US-0129845.
PR 21-APR-1999; 99US-0130077.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.

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PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 21-JUN-1999; 99US-0139899.
PR 21-JUN-1999; 99US-0140353.
PR 21-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 28-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 08-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146385.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.

PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158569.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 2.1%; Score 50; DB 21; Length 1461;
Best Local Similarity 55.1%; Pred. No. 0.0072;
Matches 98; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 981 GAACCGTGATGGAGAGCTGAACAAAGTGAAGCCCTGAAGCACTACAAATTTAGCTTACG 1040
DB 877 GAAGCAAAATGGTACGATCACCTCCCACTCCCGCTATGTGCACACTACAAATTCGCTTCG 936
QY 1041 GTTTGAAATTCGAATGAGGAAGATTATGTACTGAAATTTCTTCCAAATCCCTTTGTC 1100
DB 937 ATCGAACAACACAGCTGTTGAGTCATACGTCACCGAGAGACGTTTCTATGCGCTCGACTC 996
```

Oy	1101	TGGAACGTCCCTGTGGTGTGGTGCTCCAATATTCAAGGACTTTTGCTCCTTCTCCT	1158
D6	997	TGGTCTGTTCCTCAATCTATTTTGGGGGCTCTAACGTGCAGACTTTGTCCCTCCGCAT	1054

Search completed: April 28, 2003, 01:22:46
Job time : 502 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 01:10:31 ; Search time 2820 seconds
(without alignments)
12623.291 Million cell updates/sec

Title: US-09-913-858A-1
Perfect score: 2198
Sequence: 1 actaactcaacgtgcatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	437.6	19.9	532	13	BM143091
2	378.6	17.2	689	13	BM099511
3	337.2	15.3	571	13	BJ464838
4	332.2	15.1	517	12	BG790911
5	280.2	12.7	690	14	BQ659171
6	257.8	11.7	701	14	BQ167130

7	248.8	11.3	856	10	BEA12601
8	231.2	10.5	803	12	BF628851
9	233.8	10.2	420	9	AJ475410
10	218.8	10.0	700	9	AL503218
11	212.6	9.7	729	14	BM816799
12	208	9.5	560	14	BM737488
13	195.2	8.9	619	12	BG465531
14	191	8.7	383	13	BM443222
15	189	8.6	321	12	BG263065
16	187.2	8.5	674	13	BJ170811
17	179	8.1	844	12	BF261629
18	172.8	7.9	388	14	BQ463217
19	156.4	7.1	666	17	BM431446
20	156.4	7.1	753	17	BM418424
21	151.8	6.9	735	17	BM423619
22	146	6.6	526	9	AL500587
23	141.8	6.5	669	17	BG7847
24	136.8	6.2	772	17	BM535486
25	134.4	6.1	806	17	BM441710
26	133.8	6.1	269	10	AM695306
27	133.6	6.1	543	17	CMS00MOV
28	131.6	6.0	484	14	BM737489
29	130	5.9	496	10	AM498425
30	127.4	5.8	539	17	BM783802
31	111	5.1	529	14	BQ765453
32	110	5.0	240	9	AJ477062
33	105	4.8	604	17	AQ271924
34	105	4.8	616	17	AQ328306
35	104.6	4.8	344	17	BM440694
36	101.6	4.6	791	10	BE034958
37	101	4.6	472	12	BG241740
38	96.4	4.4	500	14	BM885010
39	89.8	4.1	568	13	BJ201098
40	86.2	3.9	235	14	BQ623003
41	84.6	3.8	433	10	AV792413
42	84.4	3.8	501	13	BI924270
43	78.6	3.6	663	17	AQ158899
44	78.6	3.6	772	17	AQ840447
45	73.8	3.4	568	17	BM776651

ALIGNMENTS

RESULT 1
BM143091
LOCUS
DEFINITION
sa139d07.y1 Gm-cl066 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl066-5150 5' similar to TR:Q9ST51 Q9ST51 FUCT C3 PROTEIN. ;
mRNA sequence.
BM143091
VERSION
KEYWORDS
SOURCE
BM143091.1 GI:17153158
EST.
soybean.
Glycine max

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM

Glycine max

REFERENCE

AUTHORS

Shoenaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corvelli, V., Khanna

1 (bases 1 to 532)
Shoenaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corvelli, V., Khanna
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
J., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoenaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

TITLE

JOURNAL

COMMENT

Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Email: est@watson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: ccu@resgen.com
 High quality sequence stop: 421.

FEATURES

source
 1. 517
 /organism="Glycine max"
 /cultivar="Williams"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl064-3675"
 /clone_lib="Gm-cl064"
 /tissue_type="seedling epicotyls"
 /dev_stage="2 week old"
 /lab_host="DH10B"
 /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
 XhoI; The cDNA library was constructed from mRNA isolated
 from the epicotyls of 2 week old seedling for the cultivar
 Williams. The seedlings were germinated in a growth
 chamber, excised above the soil level, and the plants
 were placed in a 100 ppm solution of auxin for 24 hours
 prior to harvesting. Complementary DNA was synthesized
 from mRNA using a primer consisting of a poly(dT)
 sequence with a XhoI restriction site. EcoRI adapters
 were ligated to the blunt-ended cDNA fragments followed
 by XhoI digestion. The cDNA fragments were directionally
 cloned into the EcoRI-XhoI restriction site of the
 pBluescript vector. The ligated cDNA fragments were
 transformed into DH10B host cells (GibcoBRL). This
 library was constructed in the laboratory of Dr. Randy
 Shoemaker."

BASE COUNT 147 a 88 c 110 g 172 t
 ORIGIN

Query Match 15.1%; Score 332.2; DB 12; Length 517;
 Best Local Similarity 83.7%; Pred. No. 1.1e-49;
 Matches 426; Conservative 0; Mismatches 73; Indels 10; Gaps 4;

Oy 1456 GGAAGGTTTCAGATGGAGTCCATTTACCTGAGGCTAGCATTTAACTCTGATGCGTGTG 1515
 Db 1 GGAAGGTTTCAGATGGAGTCCATTTACCTGAGGCTAGCATTTAACTCTGATGCGTGTG 60
 Oy 1516 AAGGCTCTCTGTTTGAAGTTCACATCCCTGAACTTGTGCTGTATGGAAGACTGAA 1575
 Db 61 AAGTTGCTCTGTTTGAAGTTCACATCCCTGAACTTGTGCTGTATGGAAGACTGAA 120
 Oy 1576 AGGCTGAAGTATAGAGGGGGAGTGTCTTAAACTCTACAAATATACCAATGGC 1635
 Db 121 AGACCTGAATCTTAGAGGGGGCAATGATTTAAACTCTACAAATATACCAATGGC 180
 Oy 1636 TTGACACAGACAGCAAGCTCTTATACCTTCAGCTTCAAGGTGATGCTGATTCAGGAGT 1695
 Db 181 TTGACACAGACAGCAAGCTCTTATACCTTCAGCTTCAAGGTGATGCTGATTCAGGAGT 240
 Oy 1696 CACTTGGAGAACAACTCTTGTGCGCAAGTTTGAAGTCAATTTTGTGATGAGCTGCTAAAT 1755
 Db 241 CACTTGGAGAACCACTCTTGTGCGCAAGTTTGAAGTCAATTTTGTGATGAGCTGCTAG 299
 Oy 1756 GGTACCTCTGCTTACTCAATAG--CTTCACTTAGCTGAGCACTAGCTAGAGTTTATG 1813
 Db 300 GGCTCTCTGCTCTACATGAATAGCTCTTCACTTAACTGAGC---GGTAGAGTTTATG 355
 Oy 1814 GAATGATATGGCAGTGAATATGGCATGCTTTATTTATGCTAGTTTCTTGGCCAACTC 1873
 Db 356 GGATGATATGGCAATGAACCTGGCATGCTTTATTTATGATAGCTTCTTGACCACTC 415
 Oy 1874 ATTGATCTTTGTATGACATCACTTAAATTTAACTGTTTCTGT---AAGAGTG 1930
 Db 416 ATTGATCTTTGTATGACATCACTTAAATTTAACTGTTTCTGT---AAGAGTG 475
 Oy 1931 CAATGCATATTTAATGCTTTAGTTTATG 1959
 Db 476 AGGTTCCATATTTAATGCTTTAGTTTATG 504

RESULT 5

LOCUS B0659171/c

DEFINITION

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

B0659171 HD01K22W HD Hordeum vulgare cDNA clone HD01K22 3-PRIME, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

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sequence.

ACCESSION

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TITLE

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KEYWORDS

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REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

B0659171 HD01K22W HD Hordeum vulgare cDNA clone HD01K22 3-PRIME, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

B0659171 HD01K22W HD Hordeum vulgare cDNA clone HD01K22 3-PRIME, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

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ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

B0659171 HD01K22W HD Hordeum vulgare cDNA clone HD01K22 3-PRIME, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

B0659171 HD01K22W HD Hordeum vulgare cDNA clone HD01K22 3-PRIME, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

B0659171 HD01K22W HD Hordeum vulgare cDNA clone HD01K22 3-PRIME, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

450 CCAGCAAGAGGACAGTATACCACTTATTTGTCAGAGAGAGGCGGCTTAAAGACAG 391
 QY 1472 AGTCCATTACCTGAGGCTAGCAATTAACCTGAATCTGTGAAGCTGCTGTGTTT 1531
 Db 390 AGAATTTTATCTAGATCAGATCAGTTAACTTTAGGAGCTTTGAAGTCTGCTGTCAGC 331
 QY 1532 TGAAGTTCACATCCCTGAATCTTGTGCTGTATGGAAGACTGAAGCCCTGAAGTTATAA 1591
 Db 330 ATAAATTTAGCTCCCTCAAGCATGCTCTATATGGAAGGATGAAGGCCATCAAGTATTC 271
 QY 1592 GAGGGGGAGTGTCTTAAACTCTACAAAATATACCAATTTGCTTCAGACAGACAGAAC 1651
 Db 270 GAGTGGGATGAATGGAAGTGTACAAATTTATCCAAATAGTCTTACAGAACGACAAAG 211
 QY 1652 CTCCTTTACCTTCAGCTTCAAGGTCAGCTGATTTTCAGAGATCTACTTGGAGAACATC 1711
 Db 210 CGTTATATAAATTTCAATTCAGTGCAGCTGCTGAAGTGTCTAGATATATTAAGGGCCATC 151
 QY 1712 CTGTGCCAAGTTTGAGTCAATTTTGTGTAGC 1744
 Db 150 CATGTGCAAGGCTTGAGGTGATTTTGTATATAAC 118

RESULT 6
 BQ167130/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BQ167130 701 bp mRNA linear EST 25-APR-2002
 WHE0946_F09_K18Y Wheat 5-15 DAP spike cDNA library Triticum
 aestivum cDNA clone WHE0946_F09_K18, mRNA sequence.

BQ167130
 BQ167130.1 GI:20311201
 EST.
 breed wheat.
 Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 1 (bases 1 to 701)

Anderson, O.D., Choi, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
 P.S., Hsiao, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
 Seaton, C.L. and Tong, J.C.

The structure and function of the expressed portion of the wheat
 genomes - 5-15 DAP spike cDNA library

Unpublished (2000)
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105959773
 Fax: 5105959818

Email: oandersn@pw.usda.gov
 This EST was generated by sequencing from the 3' end of the clone.
 Sequences have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20.
 Seq primer: Oligo at wobble primer (an equal mixture of (T)27A, (T
)27G and (T)27C).

FEATURES
 source

1..701
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE0946_F09_K18"
 /clone_11p="wheat 5-15 DAP spike cDNA library"
 /tissue_type="Spike"
 /dev_stage="Adult plant"
 /lab_host="E. coli SOUR"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
 greenhouse. Spikes at 5, 10 and 15 DAP were harvested,
 total RNA and poly(A) RNA were prepared, a cDNA library
 was made, and the cDNA clones were in vivo excised to
 give plus-script phagemids in the TJ Close lab (Choi,
 Close, Fenton) at the University of California.

Riverside. Plasmid DNA preparations and DNA sequencing
 were performed in the OD Anderson lab (all other authors
).

BASE COUNT 218 a 153 c 124 g 206 t
 ORIGIN
 Query Match 11.7%; Score 257.8; DB 14; Length 701;
 Best Local Similarity 68.2%; Pred. No. 1.7e-36;
 Matches 358; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

QY 1220 ATCTACAGAAAATCCCGAGCATATAATCAATTCAGCTGGAAGTATGAGGTCAT 1379
 Db 701 ATATTGCTCAATCTCTGATGCTTTTATCAATCTTTGAGGTGAAGTACCATGGTCCAT 642
 QY 1280 CTGACTCTCTCAAGGCCCTTGTGGATATGGCAGCTGTGCATTCATCGCGCTTTTSCA 1339
 Db 641 CTGATTCTTTCAAGGCACTTATTGACATGGCAGCGTTTCATTTCATCTCTGCGCTTTGCA 582
 QY 1340 TTCACTTGGCCACAGTGTAGTAGAGAGAGAAATAATCAAGCTTAAAGAGAGCTC 1399
 Db 581 TACATATCGCTACGAAGATTTCAGRAAAAGAGAAAGAACCCCAAAATTTATGAATCGCT 522
 QY 1400 CTTGCAAGTGCCTAGAGGCCAGCAACCGTATATCATATCTATGTCAGAGAAAGGGAA 1459
 Db 521 CATGTAGTTGCTCCAGCAAAAGAGGAGCAAGTATACCACTTATTTGTCAGAGAGAGAGGC 462
 QY 1460 GGTGATGATGAGTCCATTTACCTGAGTCTTAGCAATTTAACTCTCTGAATGCTGTGAAG 1519
 Db 461 GGTTTAAGACAGAGAGCAATTTATCTAAGATCAGATCACTTAACTTTAGGAGCTTTGGAGT 402
 QY 1520 CTGCTGTCTTTTGAAGTTCACTCCCTCAATCTGTGCTGCTGATGGAAGCTGAAGGC 1579
 Db 401 CTGCGTGCATGTTAATTTAGATCCCTCAAGCATGTTCTGTATGAAGATGAAGGC 342
 QY 1580 CTGAAGTTATAGAGGGGGAGTGTCTTTAAACTCTACAAAATATACCAATTTGGCTTGA 1639
 Db 341 CATCAAGTATTCGAGCGGGGATGAGTTGAAGGTGTACAAAATTTACCAATAGGCTTTA 282
 QY 1640 CACAGAGACAAAGCTCTTTTACCTTCAGCTTCAAAAGGTGATGCTGATTTCAGAGTCACT 1699
 Db 281 CAGAGACAAAGCGTTATATAATTTCAATTCAGTGTGATGCTGAAGTGTCTAGATATA 222
 QY 1700 TGGAGAACATCTCTGCGCAAGTTTGAAGTCATTTTGTGTAGC 1744
 Db 221 TTAAGGCCATCATCTGCAAGCTTGAGGTGATTTTGTGTATAAC 177

RESULT 7
 BQ12601
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BQ12601 856 bp mRNA linear EST 24-JUL-2000
 MCG002_B07B990625 ITEC MCG Barley Leaf/Culm Library Hordeum vulgare
 cDNA clone MCG002.B07, mRNA sequence.

BQ12601
 BQ12601.1 GI:9410447
 EST.
 Hordeum vulgare
 Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 1 (bases 1 to 856)

Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier
 S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
 Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P.,
 Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,
 Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,
 Sorrells, M., Warburton, M. and Wenzel, G.

International Triticale EST Cooperative (ITEC): Production of
 Expressed Sequence Tags for Species of the Triticaceae
 Unpublished (2000)

Contact: Graner A
 Institute for Plant Genetics & Crop Plant Research
 Corrensstr. 3, D-06466 Gatersleben GERMANY


```
BASE COUNT      166 a   198 c   228 g   211 t
ORIGIN
Query Match      10.5%; Score 231.2; DB 12; Length 803;
Best Local Similarity 58.5%; Pred. No. 8.8e-32;
Matches 470; Conservative 0; Mismatches 313; Indels 21; Gaps 3:
QY 269 GCTTACCCTTTTGGCTCGCGGAGGCAACCCAAAGAGAAATGAGCAATCTTAATGCTTC 328
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GCTCCACTCGCTGACCCAGGCGCAAGCCGCTCGCGCGCTCGCGGCTGCTGCCCG 60
QY 329 TTGTTGTTGCCCTTGTGTCATCGCGGAGATCGGTTTCTCGGTAGTGTGGATGCGCA 388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 TTGCTGTTGCTTCTTCTCGCGAGATCGGTTCTCTCGGTCTCGCATGTCGA 120
QY 389 AAAGCCGCCATGCTGACCTCCCTCGCTGACTTCTTCTACCGCTTCGAGCGGTGCTTG 448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 AGAACCTCAGCGGCTGAGAGCTGGACCACTCTCTCCACCGCTCTCTTCAACCTGGG 180
QY 449 AAGGTGACGATTTGGGTTGGTTTGGTGGCTTCTGATCGGAATTTCTGAATCGTATGTT 508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GCSCGATGC-----GCCTCGGGTAGCGGGGACGACGACGAGT 222
QY 509 GTGAGCAATGGTTGAGAGGAGGAGTCTGTACGCTATTCAGGGGCTTTTCCAAAGC 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 GCAGAGCGGCTTGAGAGGACGAGCGGCTGTATGACCGCGATTTTGAAGGCATC 282
QY 569 CTATTTTGTGCTGAGCTGATCAGGAGTGGAAAGTCTGTGCTGGTTGGATGTAATTTG 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 283 CTGTACTTCTGCGCGTCTGCTAAGGATTTGGAATAGATGTTCTGTAGGATGTAATTTG 342
QY 629 GGTTCAGTGGGATAGAAAGCCAGATCGCGATTTGGTGTACCTCAACCAAGTGAACAG 688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 343 GGTTCAGCTAGTAAGACGCTGATCTACTTTCGGAATCGCTCCAGATCTTCGTAG 402
QY 589 CTAGCATTTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 748
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 403 AGATATCTCTAGATCAATGGAAATGCTCTCAATATTTTCGGAACCAATTAATGCGG 462
QY 749 CAAGCGAGGGGATATACATCGTAATGACAACAGTCTATCTTCGGATGTTCTCTGTTG 808
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 463 CTCGAGGAAGAGGTTACCAAAATGTTGATGACAACAGCCTTTCTCTACATGTGCCAGTTG 522
QY 809 GATATTTTTCATGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 868
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 523 GCTACTTTTCATGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 582
QY 869 CTCTTCAGCTGCTTTTCATTTCCAAATGTTGGTGTGCTGCAAAATTTCCGGTTGCAAGCTTTG 928
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 583 GCCTAGCTGCGGCTTCATTTT-CAACTGCGGTGGCCAAAACCTTTTCGTTTGGCAGCCCTTG 641
QY 929 AGCCCTTGAAAATCAAAACATCAAAATG--ATTCTTATGTTGTTGTCACAGGAACCG 986
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 642 AGATGCTTGAAAGCTTATATGTAATAATTTGATTTCTTTGGAGCGGTTTTCGTATGG 701
QY 987 TGATGGAAGTGAACAAGTGGAGCCCTGAGCACTTACAAATTTAGCTTAGCGTTTGA 1046
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 702 TCACGCTATAGTGACAACTGCAACACCTATGGGCTCCCAATGCAAGTGGGTTCTG 761
QY 1047 AAATTCGAATGAGGAATATGT 1070
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 762 GAATTTTATGCGGATTTTGT 785

RESULT 9
AJ475410
LOCUS      AJ475410
DEFINITION AJ475410 S00008 Hordeum vulgare cdna clone S0000800035C08F1, mRNA
sequence.
ACCESSION  AJ475410
VERSION     AJ475410.1
KEYWORDS    EST.
SOURCE      Hordeum vulgare.

ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 420)
AUTHORS   Saren,A.-M., Tanskanen,J., Paulin,L. and Schulman,A.H.
TITLE     Barley EST's
JOURNAL   Unpublished (2002)
COMMENT   Contact: Schulman AH
           Institute of Biotechnology
           University of Helsinki
           P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
           Finland. Location/Qualifiers
           source          1..420
           /organism="Hordeum vulgare"
           /db_xref="taxon:4513"
           /clone="S0000800035C08F1"
           /clone_lib="S00008"
           /tissue_type="Callus"
           /note="Callus K19"
BASE COUNT      106 a   90 c   101 g   123 t
ORIGIN
Query Match      10.2%; Score 223.8; DB 9; Length 420;
Best Local Similarity 70.9%; Pred. No. 2.7e-30;
Matches 297; Conservative 0; Mismatches 122; Indels 0; Gaps 0:
QY 568 CCTATTTTGTCTGAGCTGATCAGGAGTGGAACTCGTTCGGTTGGATGTAATTT 627
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 CCTGACTTGTGCGCGTCTGCTGAAGATTGGAATAGATGTTCTGTAGGATGTAATTT 61
QY 628 GCGTTAGTGGGATACAAAGCCAGATCGCGCATTTGGTTACCTCAACCAAGTGAACA 687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 GGGTTCCAGCTAGAGACGCGCTGATCTACTTTCGGAATCGCTCCAGATCTTCCGTA 121
QY 688 GCTAGCATTTCCGATCAATGGAATCAGCAGATATCTATGCTGAGAACAAATATTGCCATG 747
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 GAGAGTATCTTCAGATCAATGGAATGCTCTCAATATTTATTCGAGAACAAATATTATCGC 181
QY 748 GCAAGCGAGGGGATATAACATCGTAATGACAACAGTCTATCTTCGGATGTTCTCTGTT 807
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 GCTCGAGGAAGGGTACCAAAATGTTGATGACAACAGCCTTCTCTCAGATGTCGAGTT 241
QY 808 GGATATTTTTCATCGGCTGAGTATGATATGATGATGATGATGATGATGATGATGATG 867
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 GGTACTTTTTCATGGGCTGAATATGATATGATATGATATGATATGATATGATATGATATG 301
QY 868 GCTCTGAGCTGCTTTTCATTTTCCAAATTTGGTGTGCTGCAAAATTTCCGGTTGCAAGCTTT 927
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 GCGTACTGCTGAGCTTTTATTTCCAACTGCGGTGCAAGAACTTCCGTTTGCAGCCCTT 361
QY 928 GAGCCCTTGAAAATCAAAACATCAAAATGATTTCTATGTTGGTGTGTCACAGGAACCG 986
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 GAGATGCTTGAAGCTTAGATATGATATGATATGATATGATATGATATGATATGATATGATATG 420

RESULT 10
AL503218
LOCUS      AL503218
DEFINITION AL503218 Hordeum vulgare Barke roots Hordeum vulgare cdna clone
HW01C14T 5', mRNA sequence.
ACCESSION  AL503218
VERSION     AL503218.1
KEYWORDS    GI:12029433
SOURCE      EST.
ORGANISM Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 700)
AUTHORS   Michalek,W., Weschke,W., Pleisner,K.-P. and Graner,A.
TITLE     EST sequencing and analysis in barley
```

JOURNAL
COMMENT

Unpublished (2000)
Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr. 3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq. primer: T3 primer for 5' end.

FEATURES

source
1. .700
Location/Qualifiers
/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/clone="HW01C147"
/clone_lib="Hordeum vulgare Barke roots"
/tissue_type="roots"
/lab_host="XLOLR"
/note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2:
XhoI; mRNA was made from roots of spring barley variety
'Barke', a high quality malting variety. Roots were grown
for two days on filter paper at room temperature. Cloning
sites: EcoRI (3'-end of cDNA) and XhoI (3'-end of cDNA).
NOTE: Due to a cloning artefact caused by the kit, in most
cases the EcoRI site is NOT present, as well as the EcoRI
adapter. Average insert size is 1 kb. Sequence trimming:
Vector sequences and sequence ends were trimmed from the
5'- and 3'-end until a 50 bp window contains less than two
ambiguities. The maximum length was set to 700 bp."
BASE COUNT 146 a 189 c 199 g 166 t
ORIGIN

Query Match 10.0%; Score 218.8; DB 9; Length 700;
Best Local Similarity 60.1%; Pred. No. 1.6e-29;
Matches 392; Conservative 0; Mismatches 242; Indels 18; Gaps 1;

Qy 269 GCTTACCGCTTTGGCTCCGGGAGGCAACCAAGAGGAATGGAGCAATCTAATGCCTC 328
Db 67 GCTCCCACTCGCTGCCAGCGGCAAGCGCTCGCGCGCTCGGGTGGCTCCCGC 126
Qy 329 TTGTTGTTGCTTGGTTCATCGCGGAGATCGCTTCTTGGTAGTTGGATATGCCCA 388
Db 127 TTGTCGTGTTGTTGTTTCTCGCGGAGATCGCTTCTCGGTGCGCTCGACATGTCGA 186
Qy 389 AAACGCGCGCATGTGACTCCCTCGCTGACTTCTTACCGCTCTCGAGCGGTGCTTG 448
Db 187 AGAACGCTGGCGGCTCGAGAGCTGACCACTCTCTCCACCGCTCTCTCAACCTGGG 246
Qy 449 AAGTGTACGATTTGGGTTGGTGGCTTCTGTGATCGGAATTCGAATCGTATAGTT 508
Db 247 GCGGGATGC-----GCCCTCGGGTAGCGGGAGCAGCAGCAAGT 288
Qy 509 GTGAGGATGCTGGAGAGGAGAGATGCTGTACATATTCAGGGGCTTTTCCAAAGAGC 568
Db 289 GCGAGGAGCGCTTGAGAGGGAGCAGCGCGTGCCTTAGCAGCGGATTTTGAAAGGCATC 348
Qy 569 CTATTTTGTCTTGGAGCTGATCAGGAGTGAAGTCTGTTCTGGTTGGATGTAATTTG 628
Db 349 CTGTACTTGTGCGCGCTGCTGCTAAGGATTGGAATAGATGTTCTGTAGGATGTGAATTTG 408
Qy 629 GGTTTACTGGGATACAAAGCCAGATGCGCATTTGGGTTACCTCAACCAAGTGAACAG 688
Db 409 GGTTCAGCTAGTACAGCCCTGATCTACTTTTCGGAATCGCTCCAGATCTTCGGTAG 468
Qy 689 CTAGCATTTGCGATCAATGGAATCAGCAGATACTATGCTGAGACAATATTTGCCATGG 748
Db 469 AGAGTATCTTCAGATCAATGGAATCGTCTCAATATTTATTCGAGACAATATTAATCGG 528
Qy 749 CAAGAGGAGGGATATAACATCGTAAGTACCAACAGTCTATCTTCGGATGTTCTCTGTTG 808
Db 529 CTCGAGGAGAGGGTACCAAAATTTGATGACACACCGCTTTCTCTAGATGTGCCAGTTG 588
Qy 809 GATATTTTCATCGGCTGAGTATGATATGATGAGGACAGTGCAGCCGCCAAACATGAAGCTG 868
Db 589 GCTACTTTTCATCGGCTGAAATATGATATCATGTCGACCTGTGCTCCCAAGACTGAAGAGG 648

Qy 869 CTCTTGACGCTGCTTTCATTTTCCAAATTTGGTCTCTCGAAATTTCCGGTTGCA 920
Db 649 CCTAGCTGCGAGCCCTTTATTTTCCAACTGCGGTGCACGAAACTTCCGTTTGCA 700

RESULT 11
BM816799
LOCUS

DEFINITION

BM816799 729 bp mRNA linear EST 05-MAR-2002
HB03F12.T3.ab1 HB Hordeum vulgare cDNA clone HB03F12.T3.ab1 similar
to (AC011807) Putative fucosyltransferase [Arabidopsis thaliana
] Fuct c3 protein [Vigna radiata] fucosyltransferase 3 [Fuct c3
protein] [Arabidopsis thaliana] g113994483[emb]CAC38048.11
(AJ404860) alpha1.3-fucosyltransferase [Arabidopsis thaliana], mRNA
sequence.

ACCESSION
BM816799
VERSION
BM816799.1 GI:19152813

KEYWORDS
EST.

SOURCE
Hordeum vulgare.

ORGANISM
Hordeum vulgare.

REFERENCE
1 (bases 1 to 729)

AUTHORS
Ozturk,N.Z., Michalowski,C.B., Brazille,S., Borchert,C., Palacio,C.
Fredrickson,M.A. and Bohnert,H.J.

TITLE
Monitoring large-scale changes in transcript abundance in drought-

JOURNAL
Unpublished (2002)

COMMENT
Contact: Mark A. Fredrickson
Plant Biology
University of Illinois
1201 W Gregory Dr, Urbana, IL 61801, USA
Tel: 217/2655473
Email: bohnertlab@life.uiuc.edu.

FEATURES
source

1. 729
/organism="Hordeum vulgare"
/strain="cv tokak"
/db_xref="taxon:4513"
/clone="HB03F12.T3.ab1"
/clone_lib="HB"
/tissue_type="Leaf"
/dev_stage="3 week old"
/note="6 and 10 hour drought stress by placing plants on
moist paper (75% rel. humidity) in light."
BASE COUNT 156 a 188 c 204 g 178 t
ORIGIN

Query Match 9.7%; Score 212.6; DB 14; Length 729;
Best Local Similarity 59.5%; Pred. No. 1.9e-28;
Matches 438; Conservative 0; Mismatches 277; Indels 21; Gaps 4;

Qy 269 GCTTACCGCTTTGGCTCCGGGAGGCAACCAAGAGGAATGGAGCAATCTAATGCCTC 328
Db 14 GCTCCCACTCGCTGCCAGCGGCAAGCGCTCGCGCGCTCGGGTGGCTCCCGC 73

Qy 329 TTGTTGTTGCCCTTTGGTTCATCGCGAGATCGCTTCTGGGTAGTTGGATATGCCCA 388
Db 74 TTGCTGTTGGTGTGCTTTTCTCGCGGAGATCGCTTCTCGGTGCGCTCGACATGTCGA 133

Qy 389 AAAACGCGCGCATGTTGACTCCCTCGCTGACTTCTTACCGCTCTCGAGCGGTGCTG 448
Db 134 AGAACGCTGCGCGGTGCGAGAGCTGGACCACTCTCTCCACCGCTCTCTTCAACCTGGG 193

Qy 449 AAGTGTACGATTTGGGGTTGGGTTGCTGGCTTCTGTATCGGAATTCGAATCGTATAGTT 508
Db 194 GCGGGATGC-----GCCCTCGGGTAGCGGGAGCAGCAGCAAGAGT 235

Qy 509 GTGAGGAATGTTGGAGAGGAGGAGTCTCTCACGCTATTTCAGAGGGCTTTTCCAAAGAGC 568
Db 236 GCGAGGAGCGCTTGAGAGGAGCAGCGCTCTGCTTACGACCGCGGATTTTCAAGAGCATC 295

COMMENT

Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Seq primer: JEN REV
 High quality sequence stop: 597
 POLYA-No.

FEATURES
source

Location/Qualifiers
 1. .619
 /organism="Sorghum propinquum"
 /db_xref="taxon:132711"
 /clone_lib="Rhizome2 (RHIZ2)"
 /note="Organ: Rhizomes; Vector: pBluescript II from Lambda
 Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
 from poly-A RNA in the cloning vector Lambda Zap II."
 Clones to be sequenced were prepared by mass excision."

BASE COUNT 123 a 165 c 196 g 135 t

Query Match 8.9%; Score 195.2; DB 12; Length 619;
 Best Local Similarity 60.3%; Pred. No. 2.7e-25;
 Matches 370; Conservative 0; Mismatches 223; Indels 21; Gaps 2;

QY 303 GAGGAATGAGCAATCAATCGCTCTGTGTTGCTTGCCTTGTGCTCATCGCGAGATCGC 362
 DB 6 CGCGCGCTGGGGTGCTGCTGCCGCTCTGTGGGCGCCCTTCTCGCCGAGATCGC 65
 QY 363 GTTCTGGGTAGTTGGATGGCCAAAGCCGCCCATGTTGACCTCCCTCGCTGACTT 422
 DB 66 GTTCTCGCGCGCTCGACATGCGGAAGACCGCGAGCGCTCGAGAGCTGGACCACTC 125
 QY 423 CTTCTACCGC-----TCTCGAGCGCTGTTCAAGTGCACATTTGGGTTGGG 470
 DB 126 CTTCTACCGCGCTCGCGCATTTGGGCGAGCGCTGGGCGGCGCCACCGAGGCG 185
 QY 471 TTTGGTGGTCTGATCG-----GAATTCGAATCGTATAGTTGTGAGGATGGTT 521
 DB 186 AGCGCGCGACGCGCGGCGAGCGAGAGATCCGCGGTTGCGGAGCGGCT 245
 QY 522 GGAGAGGAGGATGCTGTCACATATTCGAGGGGCTTTTCCAAAGAGCCTATTTTGTTC 581
 DB 246 CGAGAGGAGGAGGATGTGCTCCCTAGCAGCGGACTTTGACAGAGGATCCCGTGTG 305
 QY 582 TGGAGCTGATCAGGAGTGGAACTGCTGTTGCTGGATGTAATTTGGTTTGTGGGA 641
 DB 306 TGCGCGCGCAAGGATGGAAATAGCTATGTAGGATGCAATTTGGTTTCTCGCAG 365
 QY 642 TAGAAGCCAGATCGCGCATTTGGGTACCTCAACCAAGTGGAAACAGCTAGCATTCGCG 701
 DB 366 CAAGACACCTGATGCTACTTTTGGAAATGGCAACAGATCCCTTCTGTAGATGGTATCCTCAG 425
 QY 702 ATCAATGGATACAGAGATATCTATCTCGAGAACAAATATTTGCCATGGCAAGCGAGGGG 761
 DB 426 ATCAATGGATATCCCAATATATTTCAGAGAATAATATTGATGCTGCTCGAGGAGAGG 485
 QY 762 ATATACATCGTATGACAGACCACTATCTTCGGATGTTCTCTTGGATATTTTCATG 821
 DB 486 GTACAGATTTGTATGACCAACCGCTTCTTCAGATGTACCGATTTGGTACTTTTCATG 545
 QY 822 GGCTGATGATGATGATGCGACCACTGACGCGGAAACTGAAGCTGCTCTTGCAGCTGC 881
 DB 546 GGCTGATGATGATGATGCGACCTGTGCTCCAAAGACTGAAGAAGCTCTTGTGTCAGC 605
 QY 882 TTTCAATTCGAAT 895
 DB 606 CTTATTTCTACT 619

RESULT 14
 BM443222

LOCUS

BM443222 383 bp mRNA linear EST 23-JUL-2002
 DEFINITION EBR02_SQ003_D03_R root, 3 week, hydroponic grown, low nitrogen cv
 Optic, EBR02 Hordeum vulgare cDNA clone EBR02_SQ003_D03_5', mRNA
 sequence.

ACCESSION

BM443222

VERSION

BM443222.2 GI:21947888

KEYWORDS

EST.

SOURCE

Hordeum vulgare.

ORGANISM

Hordeum vulgare

REFERENCE

1. (bases 1 to 383)

AUTHORS

Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,
 Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.

TITLE

Development of Barley Transcriptome Resources

JOURNAL

Unpublished (2001)

COMMENT

On Feb. 1, 2002 this sequence version replaced gi:18474009.

Contact: Waugh R, Marshall DP

Genome Dynamics/Computational Biology

Scottish Crop Research Institute

Invergowrie, Dundee, DD2 5DA, Scotland, UK

Tel: 00 44 1382 562731

Fax: 00 44 1382 562426

Email: est@scri.sari.ac.uk

All sequence has a Phred quality score of 20 or over

Seq primer: M13 reverse.

Location/Qualifiers

1. .383

/organism="Hordeum vulgare"

/cultivar="Optic"

/db_xref="taxon:4513"

/clone_lib="EBR02_SQ003_D03"

cv Optic, EBR02.

/tissue_type="root, 3 week, hydroponic grown, low nitrogen,

/dev_stage="3 week"

/lab_host="DH10B"

/note="Vector: pSPOR1; Site_1: Sal I; Site_2: Not I;
 Non-normalised library, directionally cloned into pSPOR1.
 Derived from roots of 3 week old Nitrogen stressed barley
 plants. Developed as part of the barley transcriptome
 resources of BBSRC/SEERAD funded cereal IGF (Investigating
 Gene Function) project."

BASE COUNT 121 a 67 c 87 g 108 t

ORIGIN

Query Match 8.7%; Score 191; DB 13; Length 383;

Best Local Similarity 68.7%; Pred. No. 2.1e-24;

Matches 263; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1253 CATTGAGGTGGAAGTATGAGGGTCCATCTGACTCTTCAAGCCCTTGTGGATATGCGAG 1312

DB 1 CTTTGGAGTGAAGTATGATGGTCCATCTGATCTTTCAAGGCACCTTATTCACATGSCAG 60

QY 1313 CTGTGCATTCATCGTCGGCTTTGTCATTCCTTCCACAGTGTAGTAGAGAGGAAG 1372

DB 61 CGGTTCATTCCTCTGCGCTTTGTATACATATCGTCCGAAGATTCATGAAGAGAG 120

QY 1373 AAAATAATCCAGCCCTTAAGACAGCTCTTGCAGCTGCATAGAGGGCCCAAAACCGTAT 1432

DB 121 AAAAACTCCAAAATTTATGAATCGCTCGTGTAGTTGCTCCAGCAAGAGAGACAGTAT 180

QY 1433 ATCATATCTATGTTCAGAGAAAGGGGAAGTTTGGATGGAGTCCATTTACTGAGGTCTA 1492

DB 181 ACCATTATTTGTTCAGAGAGAGAGGCGGTTTAACACAGAGAACATTTATCTAAGATCAG 240

QY 1493 GCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTGTTTGAAGTTCACATCCCTGAATC 1552

DB 241 ATCAGTTAACTTTAGGAGCTTTTGAAGTCTGCTGCACAGATAAAATTTAGCTCCCTCAAGC 300

QY 1553 TTGTGCTGTATGGAAGACTGAAAGCCCTGAAAGTTATAGAGGGGGGAGTGTCTTTAAAC 1612

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-913-858A-1
Perfect score: 2198
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 1533381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/ins/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ins/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ins/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ins/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ins/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ins/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	209.4	9.5	2069	4	US-09-678-300-3
2	209.4	9.5	2124	4	US-09-678-300-6
3	209.4	9.5	2165	4	US-09-678-300-9
4	209.4	9.5	2232	4	US-09-678-300-12
5	209.4	9.5	2808	4	US-09-678-300-2
6	209.4	9.5	2863	4	US-09-678-300-5
7	209.4	9.5	2904	4	US-09-678-300-8
8	209.4	9.5	2971	4	US-09-678-300-11
9	209.4	9.5	3714	4	US-09-678-300-1
10	44.4	2.0	1639	2	US-08-737-5248-1
11	42.4	1.9	662	4	US-08-998-416-185
12	42.4	1.9	665	4	US-08-998-416-937
13	42.4	1.9	701	4	US-08-998-416-701
14	42.4	1.9	711	4	US-08-998-416-786
15	42.4	1.9	724	4	US-08-998-416-683
16	42.4	1.9	828	4	US-08-998-416-1036
17	42.4	1.9	834	4	US-08-998-416-538
18	42.4	1.9	834	4	US-08-998-416-305
19	42.4	1.9	663	4	US-08-998-416-191
20	42.4	1.9	860	4	US-08-998-416-287
21	40.6	1.8	7218	1	US-08-212-463-14
22	40.4	1.8	854	4	US-08-998-416-534
23	39.4	1.8	3573	4	US-08-353-585-4
24	38.6	1.8	6124	4	US-08-213-419B-3
25	38.2	1.7	7218	1	US-08-212-463-14
26	38	1.7	1454	1	US-08-220-958-3
27	37.8	1.7	723	2	US-08-618-911-1

28	37.8	1.7	767	4	US-08-998-416-472	Sequence 472, App
29	37.8	1.7	827	4	US-08-998-416-535	Sequence 535, App
30	37.8	1.7	1578	4	US-09-416-050A-1	Sequence 1, Appl
31	37.8	1.7	1578	4	US-09-664-800-1	Sequence 1, Appl
32	37.8	1.7	1578	4	US-09-663-309-1	Sequence 1, Appl
33	37.8	1.7	1578	4	US-09-661-569-1	Sequence 1, Appl
34	37.8	1.7	4673	1	US-07-638-431-1	Sequence 1, Appl
35	37.8	1.7	4673	5	PCT-US92-00018-1	Sequence 1, Appl
36	37.6	1.7	1371	2	US-08-428-713-1	Sequence 1, Appl
37	37.6	1.7	1371	3	US-08-904-179-1	Sequence 1, Appl
38	37.4	1.7	87350	3	US-08-781-891-79	Sequence 79, Appl
39	37.4	1.7	87543	4	US-09-791-211-3	Sequence 3, Appl
40	37.2	1.7	629	4	US-09-385-982-389	Sequence 389, App
41	36.8	1.7	1058	4	US-09-452-239-11	Sequence 11, Appl
42	36.8	1.7	1353	4	US-09-390-131-1	Sequence 1, Appl
43	36.2	1.6	2073	4	US-09-173-300-3	Sequence 3, Appl
44	36	1.6	2002	4	US-09-819-993-1	Sequence 1, Appl
45	35.8	1.6	1026	4	US-09-116-498-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-678-300-3
: Sequence 3, Application US/09678300
: Patent No. 6420548
: GENERAL INFORMATION:
: APPLICANT: VOZINA, Louis-Philippe
: APPLICANT: D'Aoust, Marc-Andr,
: APPLICANT: MEDICAGO INC.
: TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
: FILE REFERENCE: 14149-3.PCT*
: CURRENT APPLICATION NUMBER: US/09/678,300
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: US 60/157,133
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 2069
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Sequences to be used as promoter for regulating
: OTHER INFORMATION: expression of foreign genes
US-09-678-300-3

Query Match 9.5%; Score 209.4; DB 4; Length 2069;
Best Local Similarity 66.5%; Pred. No. 2.9e-51;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

Qy	1486	AGCTCTAGCAATTTAACTCTGAATGCTGGAAGGCTGCTGTTTGAAGTTCACATCC	1545
Db	170	AGATCTAGCAATTTAACTCTGAAGTCTTCAAGACTGCTGTTTACGAAGTTCACGCTC	239
Qy	1546	CTGAATCTTGTGCTGTATGGAAGACTGAAAGGCTGAAGTTATAAGAGGGGGAGTCT	1605
Db	230	CTGAATCATGCTTCTGTATGGAAGCTTGAAGACCTCAAAATCTAAAGGTGGGATAA	289
Qy	1606	TTAAACTCTACAAAATATACCAATTTGGCTTGACACAGACAGCAAGCTCTTTATACCTTC	1665
Db	290	TTGAAGTCTTACAANAATATACCTCGGGCTTGACACAGAGGCAAGCTCTTTATACCTTC	349
Qy	1666	AGCTTCAAGCTGATCTGATTTTCAGGAGTCACTTTGGAGAACAACTCTTTGCGCAAGTTT	1725
Db	350	CAGTTCACGGGAGTGTGATTTTCAGAAGTCACTTTGGAGAGCAATCTTTGTGCGCAAGTTT	409
Qy	1726	GAAGTCAATTTTGTGTAGCATGCGCTAA-----ATGCTACCTCTGCTCTACCTGAATT	1778
Db	410	GAAGTAATTTTGTGTAGCATATGTTGAGCTACCTACAAATTTACATGATCATCAGCATTT	469

APPLICANT: MEDICAGO INC.
TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
FILE REFERENCE: 14149-3*PCT*
CURRENT APPLICATION NUMBER: US/09/678,300
CURRENT FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 60/157,133
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 2863
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequences to be used as promoter for regulating
expression of foreign genes
US-09-678-300-5

Query Match 9.5% Score 209.4; DB 4; Length 2863;
Best Local Similarity 66.5%; Pred. No. 3.5e-51;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;
US-09-678-300-5

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QY 1486 AGGCTAGCAATTTAACTCTGAAGGCTGCTGTTGTTTGAAGTTTCACATCC 1545
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 909 AGATCTAGCAATTTAACTCTGGAGTCTCTCAAGACTGCTGTTCTTACGAAGTTACGTC 968
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1546 CTGAATCTTGCTGCTGATGAAGACTGAAAGGCTGAAAGCTTATAAGAGGGGAGTGC 1605
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 969 CTGAATCATGCTCTGATGAAGCTGAAAGCTGAAAGCTCAAAATCTTAAAGTGCGCATAA 1028
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1606 TTAAGACTCTACAAATATACCAATTTGGCTTGACACAGACAGACCTCTTTATACCTTC 1665
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1029 TTGAAGTTTACAAATATATACCTGCGGCTTGACACAGACAGGACGCTTTTATACCTTC 1088
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1666 AGCTTCAAGGTGATGCTGATTTGAGGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 1725
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1089 CAGTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 1148
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1726 GAAGTCATTTTGTGAGCATGCGCTAA-----ATGCTACCTCTGCTACCTGAAT 1778
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1149 GAAGTAATTTTGTGAGCATATGTTGAGCTACCTACCAATTTACATGATCAGTACGAT 1208
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1779 AGCTTCACCTAGCTGAGCAGTACGATAGTTTGAAGATGAGTATGGCAGTGAATATGGC 1838
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1209 AGCTTTTCACTTAAGTGAAGATGAAGTTTGAAGATGAGTATGACCATGGAGTCGCGC 1268
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1839 ATGGCTT-----TATTATGCTAGTTTCTTGGCCAACTCATGATGATGTTT 1884
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1269 ATGGCTTTGTAATGCTTACCTACTTTGGCCAACTCATGCGGGATTTACATTCAGAAAAT 1328
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1885 GTATAAGACATCACACTTTAAATTTTAAACTTGTCTGTAGAGTGCAATCCATATTTA 1944
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1329 ATACATGACTTCAACCATACTTAAACCCCTTTTGTGAATGAATGATGTTTATATTTA 1388
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1945 ATGCTAGTTTATGCTCTTATCTGATCATCT 1977
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1389 ATGTTGGGTTGAGTGTGTTTACTTGTATAT 1421
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 7
US-09-678-300-8
Sequence 8, Application US/09678300
Patent No. 6420548
GENERAL INFORMATION:
APPLICANT: VOZINA, Louis-Philippe
APPLICANT: D'Aoust, Marc-Andr
APPLICANT: MEDICAGO INC.
TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
FILE REFERENCE: 14149-3*PCT*
CURRENT APPLICATION NUMBER: US/09/678,300
CURRENT FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: US 60/157,133
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 2904
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequences to be used as promoter for regulating
expression of foreign genes
US-09-678-300-8

Query Match 9.5% Score 209.4; DB 4; Length 2904;
Best Local Similarity 66.5%; Pred. No. 3.5e-51;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;
QY 1486 AGCTCTAGCAATTTAACTCTCAANTGCTGTGAAGGCTGCTGTTGTTTGAAGTTTCACATCC 1545
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 909 AGATCTAGCAATTTAACTCTGGAGTCTCTCAAGACTGCTGTTCTTACGAAGTTTCACGTC 968
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1546 CTGAATCTTGCTGCTGATGAAGACTGAAAGGCTGAAAGCTTATAAGAGGGGAGTGC 1605
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 969 CTGAATCATGCTCTGATGAAGCTGAAAGCTGAAAGCTCAAAATCTTAAAGTGCGCATAA 1028
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1606 TTAAGACTCTACAAATATACCAATTTGGCTTGACACAGACAGACCTCTTTATACCTTC 1665
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1029 TTGAAGTTTACAAATATATACCTGCGGCTTGACACAGACAGGACGCTTTTATACCTTC 1088
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1666 AGCTTCAAGGTGATGCTGATTTGAGGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 1725
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1089 CAGTTCAACGGGATGTTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 1148
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1726 GAAGTCATTTTGTGAGCATGCGCTAA-----ATGCTACCTCTGCTACCTGAAT 1778
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1149 GAAGTAATTTTGTGAGCATATGTTGAGCTACCTACCAATTTACATGATCAGTACGAT 1208
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1779 AGCTTCACCTAGCTGAGCAGTACGATAGTTTGAAGATGAGTATGGCAGTGAATATGGC 1838
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1209 AGCTTTTCACTTAAGTGAAGATGAAGTTTGAAGATGAGTATGACCATGGAGTCGCGC 1268
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1839 ATGGCTT-----TATTATGCTAGTTTCTTGGCCAACTCATGATGATGTTT 1884
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1269 ATGGCTTTGTAATGCTTACCTACTTTGGCCAACTCATGCGGGATTTACATTCAGAAAAT 1328
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1885 GTATAAGACATCACACTTTAAATTTTAAACTTGTCTGTAGAGTGCAATCCATATTTA 1944
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1329 ATACATGACTTCAACCATACTTAAACCCCTTTTGTGAATGAATGATGTTTATATTTA 1388
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1945 ATGCTAGTTTATGCTCTTATCTGATCATCT 1977
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1389 ATGTTGGGTTGAGTGTGTTTACTTGTATAT 1421
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-09-678-300-11
Sequence 11, Application US/09678300
Patent No. 6420548
GENERAL INFORMATION:
APPLICANT: VOZINA, Louis-Philippe
APPLICANT: D'Aoust, Marc-Andr
APPLICANT: MEDICAGO INC.
TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
FILE REFERENCE: 14149-3*PCT*
CURRENT APPLICATION NUMBER: US/09/678,300
CURRENT FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 60/157,133
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 11
LENGTH: 2971

```
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Sequences to be used as promoter for regulating
: OTHER INFORMATION: expression of foreign genes
: US-09-678-300-11

Query Match          9.5%; Score 209.4; DB 4; Length 2971;
Best Local Similarity 66.5%; Pred. No. 3.5e-51;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGCTAGCAATTTAACTCTGAATGCTGTGAAGGCTCTCTTTTGAAGTTTCACATCC 1545
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 909 AGATCTAGCAATTTAACTCTGGAGTCTCTTCAAGACTGCTGTTCTTACGAAGTTTCAGTCC 968

QY 1546 CTGAATCTTGGCTGTATGGAAGCTGAAAGCCCTGAAGTTTATAAGAGGGGGAGTCT 1605
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 969 CTGAATCATGTTCTGTATGGAAGCCCTGAAGACTCTCAAAATTTCTAAAGGTGGCGATAA 1028

QY 1606 TTAAGAACTCTACAAATATACCCATTTGGCTTGACAGAGACAAGCTCTTTATACCTTC 1665
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1029 TTGAAGGTTTACAAATATACCTCTGGGCTTGACAGAGGCAAGCTCTTTATACCTTC 1088

QY 1666 AGCTTCAAGGTTGATGCTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 1725
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1089 CAGTTCAACGGGGATGTTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 1148

QY 1726 GAAGTCATTTTGTAGTACGCTGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1149 GAAGTAATTTTGTAGCATATGTTGAGCTACCTACATAATTTACATGATCACTGACAT 1208

QY 1779 AGCTTCACTTACGACACTAGCTAGAGTTTGTAGGAATGAGTATGCGAGTGAATATGCC 1838
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1209 AGCTTTCACCTTACTGAGAGTGAAGTTTGAAGTATGATGATGAGTATGAGTATGAGT 1268

QY 1839 ATGGCTT-----TATTTATGCTAGTTTCTTGGCCAACTCATCGGGATTTACATTCAGAAAAT 1884
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1269 ATGGCTTGTAAATGCTACCTACTTTGGCCAACTCATCGGGATTTACATTCAGAAAAT 1328

QY 1885 GTATAAGACATCACACTTTAAATTTTAAACTTTGTTCTGTAGAAGTGCATAATTCATATTA 1944
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1329 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAGATAACTGAATGTTCATATTA 1388

QY 1945 ATGCTTAGTTTGTAGTCTCTTATCTGATCATCT 1977
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1389 ATGTTGGTTGTAGTGTGTTTACTTGATTATAT 1421

RESULT 9
US-09-678-300-1
: Sequence 1, Application US/09678300
: Patent No. 6420548
: GENERAL INFORMATION:
: APPLICANT: VOZINA, Louis-Philippe
: APPLICANT: D'ARIST, Marc-Andr ,
: APPLICANT: MEDICAGO INC.
: TITLE OF INVENTION: METHOD FOR REGULATING TRANSCRIPTION OF
: FILE REFERENCE: 14149-3*PCT*
: CURRENT FILING DATE: 2000-10-03
: PRIOR FILING DATE: 1999-10-04
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 3714
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Sequences to be used as promoter for regulating
: OTHER INFORMATION: expression of foreign genes
: US-09-678-300-1
```

```
Query Match          9.5%; Score 209.4; DB 4; Length 3714;
Best Local Similarity 66.5%; Pred. No. 4.1e-51;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;

QY 1486 AGGCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTTGAAGTTTCACATCC 1545
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 909 AGATCTAGCAATTTAACTCTGGAGTCTCTTCAAGACTGCTGTTCTTACGAAGTTTCAGTCC 968

QY 1546 CTGAATCTTGGCTGTATGGAAGCTGAAAGCCCTGAAGTTTATAAGAGGGGGAGTCT 1605
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 969 CTGAATCATGTTCTGTATGGAAGCCCTGAAGACTCTCAAAATTTCTAAAGGTGGCGATAA 1028

QY 1606 TTAAGAACTCTACAAATATACCCATTTGGCTTGACAGAGACAAGCTCTTTATACCTTC 1665
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1029 TTGAAGGTTTACAAATATACCTCTGGGCTTGACAGAGGCAAGCTCTTTATACCTTC 1088

QY 1666 AGCTTCAAGGTTGATGCTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 1725
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1089 CAGTTCAACGGGGATGTTGATTTTCAAGAGTCACTTGGAGAACAACTCTTGTGCCAAGTTT 1148

QY 1726 GAAGTCATTTTGTAGTACGCTGCTAA-----ATGGTACCTCTGCTCTACCTGAAT 1778
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1149 GAAGTAATTTTGTAGCATATGTTGAGCTACCTACATAATTTACATGATCACTGACAT 1208

QY 1779 AGCTTCACTTACGACACTAGCTAGAGTTTGTAGGAATGAGTATGCGAGTGAATATGCC 1838
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1209 AGCTTTCACCTTACTGAGAGTGAAGTTTGAAGTATGATGATGAGTATGAGTATGAGT 1268

QY 1839 ATGGCTT-----TATTTATGCTAGTTTCTTGGCCAACTCATCGGGATTTACATTCAGAAAAT 1884
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1269 ATGGCTTGTAAATGCTACCTACTTTGGCCAACTCATCGGGATTTACATTCAGAAAAT 1328

QY 1885 GTATAAGACATCACACTTTAAATTTTAAACTTTGTTCTGTAGAAGTGCATAATTCATATTA 1944
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1329 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAGATAACTGAATGTTCATATTA 1388

QY 1945 ATGCTTAGTTTGTAGTCTCTTATCTGATCATCT 1977
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1389 ATGTTGGTTGTAGTGTGTTTACTTGATTATAT 1421

RESULT 10
US-08-737-524B-1
: Sequence 1, Application US/08737524B
: Patent No. 5912414
: GENERAL INFORMATION:
: APPLICANT: CARL SAVERIO FALCO
: APPLICANT: DOMINICK ANTHONY GUIDA, JR.
: APPLICANT: MARY ELIZABETH HARNETT LOCKE
: TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS, CHIMERIC
: TITLE OF INVENTION: GENES AND METHODS FOR INCREASING
: TITLE OF INVENTION: THE METHIONINE CONTENT OF THE SEEDS
: TITLE OF INVENTION: OF PLANTS
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
: STREET: 1007 MARKET STREET
: CITY: WILMINGTON
: STATE: DELAWARE
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 19898
: COMPUTER READABLE FORM:
: MEDIUM TYPE: DISKETTE, 3.50 INCH
: COMPUTER: IBM PC COMPATIBLE
: OPERATING SYSTEM: MICROSOFT WINDOWS 95
: SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/737,524B
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: LYNNE M. CHRISTENBURY
```


CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/S-30306/A/CGC1976
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 937:
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: PAG1581RP
US-08-998-416-937

Query Match 1.9%; Score 42.4; DB 4; Length 665;
Best Local Similarity 46.9%; Pred. No. 0.013;
Matches 165; Conservative 0; Mismatches 186; Indels 1; Gaps 1;
QY 1845 TTATTTATCCCTAGTTCTTGGCCCACTCATTTGTTGTATAGACATCACACTTTA 1904
DB 196 TTGATTATTATCTATTACATAAAACATTTTAAATGTTTATAAAATTAAGAATA 255
QY 1905 ATTTAAACTGTTCTCTAGAGTGCATATTTTAAATGTTTGTAGTCTCT 1964
DB 256 CTATAGAAATATTATTAATAGTATTTTAAATTTAAATTTAAATATACCATTTT 314
QY 1965 TATCTGATCATCTAGAGTGCATATTTTAAATGTTTGTAGTCTCT 2024
DB 315 TATTATAATAGATTTTAAATGTTTGTAGTCTCT 374
QY 2025 GAAGGATCAGATGTTTCACTCAAGACATTTTAAATGTTTGTAGTCTCTCGA 2084
DB 375 AATTATTAAATTTACTTCATGATATATTAATTTAAATGTTTCACTCAATATTTA 434
QY 2085 GCTTTTATAGTCTGGAAGTCTCCCTGTTGAGCACCCTGTTTGTAGTCTCT 2144
DB 435 TTTTATTAGTCTAGTAAATTTCTTATTTAAATAGTCTACCCCTTTAATGGATTTACTAC 494
QY 2145 CTGTCAGTGGTATCGTTTGTACCTCTAAATTAATATTATTAAATCTTAATA 2196
DB 495 CTACTAAATATTACTTAATAATATTATTAAATCTTAATAATA 546

RESULT 13
US-08-998-416-701
Sequence 701, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/S-30306/A/CGC1976
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 701:
SEQUENCE CHARACTERISTICS:
LENGTH: 701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: PAG1462RP
US-08-998-416-701

Query Match 1.9%; Score 42.4; DB 4; Length 701;
Best Local Similarity 46.9%; Pred. No. 0.014;
Matches 165; Conservative 0; Mismatches 186; Indels 1; Gaps 1;
QY 1845 TTATTTATCCCTAGTTCTTGGCCCACTCATTTGTTGTATAGACATCACACTTTA 1904
DB 196 TTGATTATTATCTATTACATAAAACATTTTAAATGTTTATAAAATTAAGAATA 255
QY 1905 ATTTAAACTGTTCTCTAGAGTGCATATTTTAAATGTTTGTAGTCTCT 1964
DB 256 CTATAGAAATATTATTAATAGTATTTTAAATTTAAATTTAAATATACCATTTT 314
QY 1965 TATCTGATCATCTAGAGTGCATATTTTAAATGTTTGTAGTCTCT 2024
DB 315 TATTATAATAGATTTTAAATGTTTGTAGTCTCT 374
QY 2025 GAAGGATCAGATGTTTCACTCAAGACATTTTAAATGTTTGTAGTCTCTCGA 2084
DB 375 AATTATTAAATTTACTTCATGATATATTAATTTAAATGTTTCACTCAATATTTA 434
QY 2085 GCTTTTATAGTCTGGAAGTCTCCCTGTTGAGCACCCTGTTTGTAGTCTCT 2144
DB 435 TTTTATTAGTCTAGTAAATTTCTTATTTAAATAGTCTACCCCTTTAATGGATTTACTAC 494
QY 2145 CTGTCAGTGGTATCGTTTGTACCTCTAAATTAATATTATTAAATCTTAATA 2196
DB 495 CTACTAAATATTACTTAATAATATTATTAAATCTTAATAATA 546

RESULT 14
US-08-998-416-786
Sequence 786, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709

NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwalls Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 786:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1504UP
US-08-998-416-786

Query Match 1.9%; Score 42.4; DB 4; Length 711;
Best Local Similarity 46.9%; Pred. No. 0.014;
Matches 165; Conservative 0; Mismatches 186; Indels 1; Gaps 1;
Qy 1845 TTATTTAGCTAGTTCTTGGCCAACTCATTTGTTGTATAGACATCACACTTTA 1904
Db 197 TTGATTATTATCTATTAAACATAAAACATTTTAAATGTTATAAATAAAGAAATTA 256
Qy 1905 ATTTTAACTTGTTCGTAGAGTCAATCCATTTAATGCTTAGTTTACTGCTCT 1964
Db 257 CTATAGAAATTTTAAATAGTAGTATTATTTAATTTAAT-ATTAATATACCATTTT 315
Qy 1965 TATCTGATCATCTAGAGTCAAGTCTTGTATATTTGAGTGAAGAACTGAAATCTAATA 2024
Db 316 TATTAATAAATAGATTATTAAAGTTTATTAATTAATTAAGTGATATATAATTTAATTTATATA 375
Qy 2025 GAAGGATCAGATGTTTCACCTCAAGACACATTTATTTACTTCATGTTGTTTGTATGATCTCGA 2084
Db 376 AATTATTAAATTTACTTCATTCATATATATATTAATTAATGACCTTCATATATTTA 435
Qy 2085 GCTTTTATGCTGCTGGAAGTCTCCCTGCTGTTGTTGACACCTGTTTATGCTTCAGTCTTA 2144
Db 436 TTTTATATGCTGAGTAATTTCTTATTTAATAGTCTACCCCTTTAAATGGGATATTACTAC 495
Qy 2145 CTGTCCAGTGGTATCGTTTGTGACCTCTAAAGAACTTAAATGATCTAATAA 2196
Db 496 CTACTAAATTTTACCTAATAATATATTTAATTAAGAACTTAAATCTAATAA 547

RESULT 15
US-08-998-416-683
Sequence 683, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter

APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebeschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwalls Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 683:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1453RP
US-08-998-416-683

Query Match 1.9%; Score 42.4; DB 4; Length 724;
Best Local Similarity 46.9%; Pred. No. 0.014;
Matches 165; Conservative 0; Mismatches 186; Indels 1; Gaps 1;
Qy 1845 TTATTTAGCTAGTTCTTGGCCAACTCATTTGTTGTATAGACATCACACTTTA 1904
Db 196 TTGATTATTATCTATTAAACATAAAACATTTTAAATGTTATAAATAAAGAAATTA 255
Qy 1905 ATTTTAACTTGTTCGTAGAGTCAATCCATTTAATGCTTAGTTTACTGCTCT 1964
Db 256 CTATAGAAATTTTAAATAGTAGTATTATTTAATTTAAT-ATTAATATACCATTTT 314
Qy 1965 TATCTGATCATCTAGAGTCAAGTCTTGTATATTTGAGTGAAGAACTGAAATCTAATA 2024
Db 315 TATTAATAAATAGATTATTAAAGTTTATTAATTAATTAAGTGATATATAATTTAATTTATATA 374
Qy 2025 GAAGGATCAGATGTTTCACCTCAAGACACATTTATTTACTTCATGTTGTTTGTATGATCTCGA 2084
Db 375 AATTATTAAATTTACTTCATTCATATATATATTAATTAATGACCTTCATATATTTA 434
Qy 2085 GCTTTTATGCTGCTGGAAGTCTCCCTGCTGTTGTTGACACCTGTTTATGCTTCAGTCTTA 2144
Db 435 TTTTATATGCTAGTAATTTCTTATTTAATAGTCTACCCCTTTAAATGGGATATTACTAC 494
Qy 2145 CTGTCCAGTGGTATCGTTTGTGACCTCTAAAGAACTTAAATGATCTAATAA 2196
Db 495 CTACTAAATTTTACCTAATAATATATTTAATTAAGAACTTAAATCTAATAA 546

Search completed: April 28, 2003, 03:45:53
Job time : 157 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 01:14:21 ; Search time 239 Seconds

(without alignments)
10007.142 Million cell updates/sec

Title:

US-09-913-858A-1

Perfect score:

2198

Sequence: 1 actaactcaacgctgatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	84.2	3.8	287	10	US-09-294-093B-5780
2	83.4	3.8	273	10	US-09-578-574-7836
3	49.2	2.2	477	9	US-09-918-995-2051
4	41.2	1.9	1373	10	US-09-960-352-12673
5	41	1.9	4065	10	US-09-925-301-133
6	41	1.9	4065	10	US-09-925-302-245
7	40.2	1.8	1184	9	US-10-123-155-412
8	40.2	1.8	1942	10	US-09-731-872-43
9	39	1.8	1446	10	US-09-764-853-180
10	39	1.8	1446	10	US-09-764-853-370
11	38.8	1.8	2523	10	US-09-861-451A-29
12	38.6	1.8	873	10	US-09-770-445-553
13	38.2	1.7	386	10	US-09-770-791-77
14	38.2	1.7	473	10	US-09-960-352-6407
15	38	1.7	345	10	US-09-770-791-772
16	38	1.7	4298	9	US-09-997-672-1
17	38	1.7	4921	9	US-09-997-672-2
18	37.8	1.7	375	10	US-09-960-352-15014
19	37.8	1.7	413	10	US-09-924-035A-435

20	37.8	1.7	1566	10	US-09-974-300-1166	Sequence 1166, Ap
21	37.8	1.7	1613	10	US-09-745-763-78	Sequence 78, Appl
22	37.6	1.7	1435	10	US-09-732-618-15	Sequence 15, Appl
23	37.6	1.7	2022	9	US-09-955-999-56	Sequence 56, Appl
24	37.6	1.7	2756	9	US-09-963-234-1	Sequence 1, Appl
25	37.4	1.7	617	10	US-09-764-877-121	Sequence 121, App
26	37.4	1.7	812	10	US-09-770-445-770	Sequence 770, App
27	37.4	1.7	1079	10	US-09-770-445-126	Sequence 126, App
28	37.4	1.7	1461	9	US-10-080-960-3	Sequence 3, Appl
29	37.4	1.7	1669	9	US-10-080-960-1	Sequence 1, Appl
30	37.4	1.7	1947	10	US-09-864-761-4439	Sequence 1439, Ap
31	37	1.7	277	10	US-09-960-352-12673	Sequence 12673, A
32	37	1.7	418	9	US-09-918-995-7350	Sequence 7350, Ap
33	37	1.7	2290	10	US-09-822-849A-152	Sequence 152, App
34	36.8	1.7	215	10	US-09-960-352-5093	Sequence 5093, Ap
35	36.8	1.7	500	9	US-09-918-995-23879	Sequence 23879, A
36	36.8	1.7	1024	9	US-10-123-155-198	Sequence 198, App
37	36.8	1.7	1058	10	US-09-452-239-11	Sequence 11, Appl
38	36.6	1.7	431	10	US-09-960-352-5558	Sequence 5558, Ap
39	36.6	1.7	689	9	US-10-001-883-3	Sequence 3, Appl
40	36.6	1.7	2000	9	US-09-938-842A-3564	Sequence 3564, Ap
41	36.6	1.7	2000	10	US-09-887-576-112	Sequence 112, App
42	36.4	1.7	308	10	US-09-960-352-7670	Sequence 7670, Ap
43	36.2	1.6	193	10	US-09-867-701-9750	Sequence 9750, Ap
44	36.2	1.6	257	10	US-09-887-576-609	Sequence 609, App
45	36.2	1.6	1401	10	US-09-925-301-410	Sequence 410, App

ALIGNMENTS

RESULT 1

US-09-294-093B-5780

; Sequence 5780, Application US/09294093B

; Patent No. US20010051335A1

; GENERAL INFORMATION:

; APPLICANT: Lalqudi, Raghunath, V.

; APPLICANT: Ito, Laura, Y.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

; FILE REFERENCE: PL-0009 US

; CURRENT APPLICATION NUMBER: US/09/294, 093B

; CURRENT FILING DATE: 1999-04-16

; PRIOR APPLICATION NUMBER: 60/082,567

; PRIOR FILING DATE: April 21, 1998

; NUMBER OF SEQ ID NOS: 6207

; SOFTWARE: PERL Program

; SEQ ID NO 5780

; LENGTH: 287

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20010051335A1 700382332H1

US-09-294-093B-5780

Query Match 3.8%; Score 84.2; DB 10;

Best Local Similarity 67.2%; Pred. No. 1.5e-13;

Matches 119; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy	658	GCATTTCGGTTACTCAACCAAGTGAACAGTAGCATTCTCGGATCAATCGAATCAGCA 717
Db	39	GGATGGGTAATGCTACATCTTCTGTAGAGGGTATCTTCGGGATCAATGGAATCATCT 98
Qy	718	GAATATCTATGCTGCAACAAATATTCATGCGAAGCAGGAGGATATACATGCTGAATG 777
Db	99	CAATATTTATTAAGAATAGTATTGATGCTGCGAGGAGGAGGATCAAGATTGTGATG 158
Qy	778	ACAACCACTATCTTCGGGATGTCCTGTTGGATATTTTCATGGCTGACTGAT 834
Db	159	ACATGACGCTTTCTTCACACAGTCCAGTTGGCTACTCTTCATGGGCTGAATATGAT 215


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QY 2118 TGACCACTCTTATTCCTCAGTGTACTGTCAGTGGTTATCGTTTGTGACCTCTAAAA 2177
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 89 CAAGTACCTGAATTTGAATGAAGTCTATTTTGAATAAATAAAGTCTAGAACTCTTAA 30
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2178 AAAAAAAAAAAAAAAAAAAAAA 2198
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 29 AAAAAAAAAAAAAAAAAAAAAA 9
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-09-861-451A-29
: Sequence 29, Application US/09861451A
: Patent No. US2002006828A1
: GENERAL INFORMATION:
: APPLICANT: Commonwealth Scientific & Industrial Research Orga
: TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences
: FILE REFERENCE: FF34033/01
: CURRENT APPLICATION NUMBER: US/09/861,451A
: PRIOR FILING DATE: 2001-05-21
: PRIOR APPLICATION NUMBER: PP7273
: NUMBER OF SEQ ID NOS: 84
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 29
: LENGTH: 2523
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Clone pad742
US-09-861-451A-29

Query Match 1.8%; Score 38.8; DB 10; Length 2523;
Best Local Similarity 50.5%; Pred. No. 4.6;
Matches 94; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1022 ACTACAAATTTAGCTGCTTGAATTCGAATGAGGAGATATGTAAGTCACTGAAAT 1081
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Db 1820 ATTACAAGACAATATGAATTTTAAATTTACAAATTTACGAAATATTTATCCCAAAAT 1879
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1082 TCTTCCAACTCCCTGTGTGGAACGTCCCTGTGTTGTGCTCCAAATATTCAGG 1141
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1880 ACAGTCTAACTTTTGAAGCGCAGCTCAAAAATATGAACTTCAATCCAGAAAAAGATG 1939
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1142 ACTTGTCTCTCTCTGTTCAATTTTACATATTAAAGATAGAGATGTTGAGTCTG 1201
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1940 CTCGCAATTTGTTAATAGTCTAAATTTAGAGATTAAGCGCTTGGAAATGTTAATTAG 1999
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1202 TTGCAA 1207
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Db 2000 ATGCAA 2005
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RESULT 12
US-09-770-445-553/c
: Sequence 553, Application US/09770445
: Patent No. US20020023281A1
: GENERAL INFORMATION:
: APPLICANT: Goriach, Jorn
: APPLICANT: An, Yong-Qiang
: APPLICANT: Hamilton, Carol M.
: APPLICANT: Price, Jennifer L.
: APPLICANT: Raines, Tracy M.
: APPLICANT: Yu, Yang
: APPLICANT: Rameaka, Joshua G.
: APPLICANT: Page, Amy
: APPLICANT: Ledford, Brooke L.
: APPLICANT: Woessner, Jeffrey P.
: APPLICANT: Haas, William David
: APPLICANT: Krickler, Maja
: APPLICANT: Slader, Ted
```

```
: APPLICANT: Davis, Keith R.
: APPLICANT: Allen, Keith
: APPLICANT: Hoffman, Neil
: APPLICANT: Hurlban, Patrick
: TITLE OF INVENTION: Expressed Sequences of Arabidopsis
: TITLE OF INVENTION: thaliana
: FILE REFERENCE: 202305 (PARA-012PRV)
: CURRENT APPLICATION NUMBER: US/09/770,445
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: US 60/178,472
: NUMBER OF SEQ ID NOS: 999
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 553
: LENGTH: 873
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-770-445-553

Query Match 1.8%; Score 38.6; DB 10; Length 873;
Best Local Similarity 52.9%; Pred. No. 2.5;
Matches 83; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 2040 TCACCTCAAGACACATTTACTTCTATCTGTTTGTGATGATCTCGACCTTTTGTAGTGTCT 2099
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 157 TTACTAAACAGTTCCTCCATACCTTTTGTGTTGTTTCTTACTTTAGTTTCTGCTT 98
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2100 GGAAGTGTCCCTGTGTTGAGCACCTGTTATGCTTCAGTGTCTACTGTCAGTGTGTTAT 2159
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 97 TCTTCTGTATGTTGTTTAGAGATTTTGTGTTTCTTGAGATTTTGTGAGATTTGCGTTC 38
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2160 CTTTTTGCACCTCTAAAAAAAAAAAAAAAAAAAAAAA 2196
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 37 ATATTATGAACTTAGGTTATGTAAGAAAAA 1

RESULT 13
US-09-770-791-77
: Sequence 77, Application US/09770791
: Patent No. US20020062014A1
: GENERAL INFORMATION:
: APPLICANT: Goriach, Jorn
: APPLICANT: An, Yong-Qiang
: APPLICANT: Hamilton, Carol M.
: APPLICANT: Price, Jennifer L.
: APPLICANT: Raines, Tracy M.
: APPLICANT: Yu, Yang
: APPLICANT: Rameaka, Joshua G.
: APPLICANT: Page, Amy
: APPLICANT: Ledford, Brooke L.
: APPLICANT: Woessner, Jeffrey P.
: APPLICANT: Haas, William David
: APPLICANT: Krickler, Maja
: APPLICANT: Slader, Ted
: APPLICANT: Davis, Keith R.
: APPLICANT: Allen, Keith
: APPLICANT: Hoffman, Neil
: APPLICANT: Hurlban, Patrick
: TITLE OF INVENTION: Expressed Sequences of Arabidopsis
: FILE REFERENCE: 2029 (PARA-018PRV)
: CURRENT APPLICATION NUMBER: US/09/770,791
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/178,480
: NUMBER OF SEQ ID NOS: 999
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 77
: LENGTH: 386
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
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US-09-770-791-77

	Query Match	1.7%	Score 38.2;	DB 10;	Length 386;
	Best Local Similarity	55.7%;	Pred. No. 1.9;		
Matches	73; Conservative	0;	Mismatches	58; Indels	0; Gaps
OY	2067 TTGTTTGTATGCACAGCTTTTTTAGTGTCGAACTGCCCTCGCTGGTTGACCACT	2126			
Dd	256 TTCGTGGTGTGTCACATTCCAGACTATTATCCTCTCTTTCTTTGATGTATAAATCT	315			
OY	2127 GTATTGCTTCACTGTTACTGTCACCAGTGTTATCGTTTTGACCTCTAAAAAAAAAAAAAAA	2186			
Dd	316 GTGACATTCCAGTCTGTAAATATTTTGGACTTAGGTTTCAAATTTCAAAAAAAAAAAAA	375			
OY	2187 AAAAAAAAAAAAAA	2197	{ } { } { } { }		
Dd	376 AAAAAAAAAAAAAA	386	{ } { } { } { }		

RESULT 14
 US-09-960-352-6407
 : Sequence 6407, Application US/09960352
 : Patent No. US20020137139A1
 : GENERAL INFORMATION:
 : APPLICANT: Warren, Wesley C.
 : APPLICANT: Tao, Nengbing
 : APPLICANT: Byatt, John C.
 : APPLICANT: Mathialagan, Nagappan
 : TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 : FILE REFERENCE: 16511.006/37-21(10298)C
 : CURRENT APPLICATION NUMBER: US/09/960,352
 : CURRENT FILING DATE: 2001-09-24
 : NUMBER OF SEQ ID NOS: 15112
 : SEQ ID NO 6407
 : LENGTH: 473
 : TYPE: DNA
 : ORGANISM: Bos taurus
 : OTHER INFORMATION: Clone ID: 28-BovMS1-003-Q1-E1-G7
 US-09-960-352-6407

Query Match	1.7%	Score 38.2;	DB 10;	Length 473;
Best Local Similarity	53.7%	Pred. No. 2.1;		
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Gaps	0;			

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QY	2110	CTGTGTTGTTGAGCACCCTGTTATGCTCAGT	TGTTACTGTCTAC	CGCTGCTT	ATCGTTTT	TTCAGC	2169
Db	94	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	153
QY	2170	CTCTAAAAA	AAAAAAAAAAAAA	AAAAA	AAAAA	AAAAA	2196
Db	154	TTTTTAAAAA	AAAAAAAAAAAAA	AAAAAAAAA	AAAAA	AAAAA	180

RESULT 15
US-09-770-791-772/c
: Sequence 772, Application US/09770791
: Patent No. US20020062014A1
: GENERAL INFORMATION:
: APPLICANT: Gorfach, Jörn
: APPLICANT: An, Yong-Qiang
: APPLICANT: Hamilton, Carol M.
: APPLICANT: Price, Jennifer L.
: APPLICANT: Raines, Tracy M.
: APPLICANT: Yu, Yang
: APPLICANT: Rameaka, Joshua G.
: APPLICANT: Page, Amy
: APPLICANT: Matthew, Abraham V.
: APPLICANT: Leadford, Brooke L.

```

: APPLICANT: Woessner, Jeffrey P.
: APPLICANT: Haas, William David
: APPLICANT: Garcia, Carlos A.
: APPLICANT: Krickler, Maja
: APPLICANT: Slader, Ted
: APPLICANT: Davis, Keith R.
: APPLICANT: Allen, Keith
: APPLICANT: Hoffman, Neil
: APPLICANT: Hurban, Patrick
: TITLE OF INVENTION: Expressed Sequences of ArabidopsIs
: FILE REFERENCE: 2029 (PARA-018PRV)
: CURRENT APPLICATION NUMBER: US/09/770,791
: CURRENT FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/178,480
: PRIOR FILING DATE: 2000-01-27
: NUMBER OF SEQ ID NOS: 999
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 772
: LENGTH: 345
: TYPE: DNA
: ORGANISM: ArabidopsIs thaliana
: US-09-770-791-772

Query Match          1.7%   Score 38; DB 10; Length 345;
Best Local Similarity 71.4%; Pred. No. 2;
Matches 50; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Db 88 TAAATCTTTTGTGTTTTTAATCTCAAGATGCTAATAATTTATGATCTTCACATAAAAAA 29

QY 2189 AAAAAAANA 2198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28 AAAAAAANA 19

Search completed: April 28, 2003, 03:50:05
Job time : 279 secs

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2003, 00:45:31 : Search time, 5603 seconds
(without alignments)
11416.735 Million cell updates/sec

Title: US-09-913-858a-1
Perfect score: 2198
Sequence: 1 actaactcaacgtgcatt.....aaaaaaaaaaaaaaaaaaaaa 2198

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
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- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
- 35: em.htg_rod.*
- 36: em.htg_nam.*
- 37: em.htg_vrt.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2198	100.0	2198	6	AX033383	AX033383 Sequence
2	2191.6	99.7	2198	8	VRA18529	V18529 Vigna radia
3	690	31.4	1506	8	ATH404860	AJ404860 Arabidops
4	690	31.4	1729	8	ATH345084	AJ345084 Arabidops
5	678.8	30.9	1542	8	ATH345085	AJ345085 Arabidops
6	678.8	30.9	1938	8	AY054522	AY054522 Arabidops
7	664.8	20.2	1824	8	ATH404861	AJ404861 Arabidops
8	534	24.3	658	8	MTR416755	AJ416755 Medicago
9	349	15.9	787	8	AF277228	AF277228 Arabidops
10	346	15.7	588	8	AF277229	AF277229 Arabidops
11	209.4	9.5	2069	6	AX105537	AX105537 Sequence
12	209.4	9.5	2124	6	AX105540	AX105540 Sequence
13	209.4	9.5	2165	6	AX105543	AX105543 Sequence
14	209.4	9.5	2232	6	AX105546	AX105546 Sequence
15	209.4	9.5	2808	6	AX105536	AX105536 Sequence
16	209.4	9.5	2883	6	AX105539	AX105539 Sequence
17	209.4	9.5	2904	6	AX105542	AX105542 Sequence
18	209.4	9.5	2971	6	AX105545	AX105545 Sequence
19	209.4	9.5	3714	6	AX105535	AX105535 Sequence
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21	171	7.8	81875	8	AP000419	AP000419 Arabidops
22	155	7.1	89134	2	AP004162	AP004162 Oryza sat
23	155	7.1	141717	2	AP004457	AP004457 Oryza sat
24	105	4.8	105	6	AX033385	AX033385 Sequence
25	60.2	2.7	1449	8	BVU315848	AJ315848 Beta vulg
26	60	2.7	1630	8	LES313193	AJ313193 Lycopersi
27	54.6	2.5	177674	2	AC127920	AC127920 Rattus no
28	54.6	2.5	190304	2	AC114439	AC114439 Rattus no
29	53.4	2.4	97683	2	AC116548	AC116548 Dictyoste
30	53.4	2.4	234488	2	AC109698	AC109698 Rattus no
31	53	2.4	807	8	MTR416757	AJ416757 Medicago
32	51.8	2.4	188464	9	AC096757	AC096757 Homo sapi
33	50.6	2.3	122160	2	CNS074PV	AL731761 Oryza sat
34	50	2.3	1149	3	CEL505020	AJ505020 Caenorhab
35	50	2.3	39370	3	AC006674	AC006674 Caenorhab
36	50	2.3	180664	2	AC006706	AC006706 Caenorhab
37	50	2.3	183800	2	AC123118	AC123118 Rattus no
38	49.8	2.3	11109	2	AC121599	AC121599 Mus muscu
39	49.6	2.3	1128	10	AF345993	AF345993 Rattus no
40	49.4	2.2	1182	8	AY026941	AY026941 Arabidops
41	49.4	2.2	1209	8	ATH404862	AJ404862 Arabidops
42	49.4	2.2	56956	2	AC117081	AC117081 Dictyoste
43	49.4	2.2	80413	8	AC021665	AC021665 Arabidops
44	49.2	2.2	1479	6	AX356085	AX356085 Sequence
45	49.2	2.2	2408	9	AK095482	AK095482 Homo sapi

ALIGNMENTS

RESULT 1	AX033383	Sequence 1 from Patent WO0049153.	2198 bp	DNA	linear	PAT 21-SEP-2000
AX033383	LOCUS	Sequence 1 from Patent WO0049153.				
AX033383	DEFINITION	Sequence 1 from Patent WO0049153.				
AX033383	ACCESSION	AX033383				
AX033383	VERSION	AX033383.1	GI:10280157			
AX033383	KEYWORDS	unidentified.				
AX033383	SOURCE	unidentified.				
AX033383	ORGANISM	unclassified.				
AX033383	REFERENCE	1 (bases 1 to 2198)				
AX033383	AUTHORS	Altman, F.				
AX033383	TITLE	Fucosyl transferase gene				
AX033383	JOURNAL	Patent: WO 0049153-A.1 24-AUG-2000;				
AX033383		ALTMANN FRIEDRICH (AT)				

FEATURES		Location/Qualifiers									
source	1. .2198										
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ORIGIN											
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	Best Local Similarity	100.0%	Pred. No. 0;								
	Matches 2198;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps			
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Db	1	ACTAACTCAACGCTGCATTTCTTTTCTTCAGGGAAACCATCCACCCCAATAACAACAA	60								
Qy	61	AAAAACACACGACGAGCTGTGTGTATCGTCTCTTTTCTTTAAACAGCACCCCA	120								
Db	61	AAAAACACACGACGAGCTGTGTGTATCGTCTCTTTTAAACAGCACCCCA	120								
Qy	121	TCATGGAATCGTGTCTAATACGGCCAAATTTTCCATTTCCTTTGATTTTACGTTATTT	180								
Db	121	TCATGGAATCGTGTCTAATACGGCCAAATTTTCCATTTCCTTTGATTTTACGTTATTT	180								
Qy	181	TCGGGAATTCGGAGTTGGGGCGGCAATGATGATGGGTCTGTGTACGAATCTTTCGAGGC	240								
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Qy	541	ACGTATTCGAGGGGCTTTCCAAAGACCTATTTTTGTTCTCGAGCTGATCAGGAGTGG	600								
Db	541	ACGTATTCGAGGGGCTTTCCAAAGACCTATTTTTGTTCTCGAGCTGATCAGGAGTGG	600								
Qy	601	AAGTCGTTCGGTTGGATGTAAATTTGGGTTTACTGGGGATAGAAAGCCAGATGCCCA	660								
Db	601	AAGTCGTTCGGTTGGATGTAAATTTGGGTTTACTGGGGATAGAAAGCCAGATGCCCA	660								
Qy	661	TTTGGGTTACCTCAACCAAGTGGACAGCTAGCATTCGCGATCAATGGAATCAGCAGAA	720								
Db	661	TTTGGGTTACCTCAACCAAGTGGACAGCTAGCATTCGCGATCAATGGAATCAGCAGAA	720								
Qy	721	TACTATGCTGAGACATATTTGCCATTCGCAACGAGGGGATATACATCTCGTAATGACA	780								
Db	721	TACTATGCTGAGACATATTTGCCATTCGCAACGAGGGGATATACATCTCGTAATGACA	780								
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Db	781	ACCAGTCTATCTCCGGATGTTCTGTGTGGATATTTTTCATGGCTGAGTATGATATGATG	840								
Qy	841	GCACAGTGCACCGGAAACTGAGCTGCTTTCAGCTGCTTTCATTTCCAATTTGCT	900								
Db	841	GCACAGTGCACCGGAAACTGAGCTGCTTTCAGCTGCTTTCATTTCCAATTTGCT	900								
Yy	901	GCTCGAAATTTCCGGTTGCAAGCTCTTTGAGCGCCCTTGAATAATCAAAATCAAAATTTGAT	960								

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Db 1981 AGTCACAGTCTTGATATATTGTGAGTGAAACTGAATCTAATAGAGGATCAGATGTTT 2040
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Db 2101 GAACTGTCCTGCTGTTGACACACTGTTATTGCTTCAGTGTACTGTCAGTGGTTATC 2160
Qy 2161 GTTTTTCACCTCTAAAAAANAAAAAAAAAAAAAAAAAAAAA 2198
Db 2161 GTTTTTCACCTCTAAAAAANAAAAAAAAAAAAAAAAAAAAA 2198

RESULT 2
VRA18529
LOCUS      Vigna radiata mRNA for alpha-1,3-fucosyltransferase (Fuct c3).
DEFINITION      Vigna radiata var. radiata
ACCESSION      Y18529
VERSION        Y18529.1 GI:5702038
KEYWORDS       alpha-1,3-fucosyltransferase; fuct gene; GDP-L-Fuc.
SOURCE        mung bean.
ORGANISM       Vigna radiata var. radiata
REFERENCE      1
AUTHORS        Leiter, H., Mucha, J., Staudacher, E., Grimm, R., Glossl, J. and
                Altman, F.
TITLE          Purification, cDNA cloning, and expression of GDP-L-Fuc:Asn-linked
                GlcNAc alpha1,3-fucosyltransferase from mung beans
JOURNAL        J. Biol. Chem. 274 (31), 21830-21839 (1999)
MEDLINE        99348317
PUBMED        10419500
REFERENCE      2 (bases 1 to 2198)
AUTHORS        Mucha, J.
TITLE          Direct Submission
JOURNAL        Submitted (10-DEC-1998) J. Mucha, Institut.fuer Chemie, Universitaet
                fuer Bodenkultur Wien, Muthgasse 18, 1190 Wien, Austria
FEATURES
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                AFENSNEDYVTEKFOSLVAGTPVVPVVGAPNIQDFAPSPGSLIHLKEIEDVESVAKT
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                LARRCKTRGPETVHYIYVRERGFEMESIYLRSSNLNLINAVKAAVLUKFTSLMDVP
                VKMTERPEVNGSALKLYIKIYIGLITQROALYTFKGDADFRSHLENNPYAKFEVI
                FV"
BASE COUNT     595 a 412 c 516 g 675 t
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Query Match    99.7%; Score 2191.6; DB 8; Length 2198;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2194; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ACTCACTCAAAACGCTGCATTTCTTTTCTTCAGGGAACCATCCACCCCAACAACAA 60

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Qy	733	AA	CA	AT	TT	GC	CA	TG	CG	CA	AG	CG	GA	TT	AT	TA	AC	AT	CT	AT	AT	GA	CA	CA	CG	AT	CT	AT	CT	792
Db	496	AA	TA	AT	CT	TG	CT	CA	AG	CG	AC	GA	AG	GT	TAT	GAT	TAT	CT	GT	AT	GA	CA	CA	CT	AT	GT	CT	GT	CA	555
Qy	793	TC	GG	AT	TT	CC	CT	GT	TG	GA	TAT	TT	TC	AT	GG	CT	GA	GT	AT	GAT	AT	GT	AT	GC	CA	CG	AG	CT	GC	852
Db	556	TC	AG	AT	TT	CC	CT	GT	TG	GG	TAT	TT	TC	AT	GG	CG	GA	AT	GAT	AT	TAT	AT	GG	CT	CA	CG	AT	GC	CA	615
Qy	853	CC	GA	AA	CT	GA	AG	CT	GC	TT	CT	TC	CA	TT	TC	CA	AT	TT	GG	CT	GC	CA	AA	AT	TC	CA	AA	AT	TC	912
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Db	676	CG	CT	TC	CA	AG	CT	TC	TG	AA	GC	CT	TAT	GA	AG	AC	GA	AT	CT	T	AA	GT	AT	GAT	TC	TT	AT	GC	TG	735
Qy	973	TG	TC	CA	GA	AA	CC	GT	GA	TG	GA	AG	TG	CA	AA	AG	CG	CC	CT	GA	AG	CA	CT	GA	CA	CA	AA	AT	TC	1032
Db	736	TG	TC	AC	CG	CA	TT	CG	GA	TG	GG	AG	TG	TG	GA	AG	GT	TC	GA	AG	GT	TC	TA	AG	CA	CT	GA	CA	AT	795
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Db	856	CT	AG	TC	CG	CT	GG	AT	CT	GT	CC	CT	GT	GG	TT	TG	GG	AG	CT	CC	AA	AT	TAT	GA	GA	AA	AT	TT	GC	915
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Qy	1213	AT	CA	GA	TAT	CT	TA	GA	CA	AA	AT	TC	CG	CA	AG	CA	TAT	AT	CA	AT	TAT	AG	GT	GG	AG	AT	GA	TG	1272	
Db	976	AT	GA	AG	TAT	CT	TT	GG	CG	AT	CA	CC	CT	TAT	AT	CT	GA	AG	CT	TAT	AG	AT	GG	AA	CA	AT	GA	AA	1035	
Qy	1273	GG	TC	CA	TG	ACT	TC	CT	TC	CA	AG	CC	CT	TG	TG	GA	TAT	AG	CA	GT	CT	GC	AT	TC	AT	CT	GC	GC	1332	
Db	1036	GG	CC	CT	TC	AG	AT	CT	TT	TT	TA	AG	CA	CT	TAT	TG	AT	TG	GC	TG	CT	CT	TA	CA	CT	CT	CT	GC	1095	
Qy	1333	CT	TT	GC	ATT	TC	ACT	TG	CC	CA	CA	AG	TG	AG	TAG	AG	AA	GA	AA	AA	TAT	CA	AA	GC	TT	TA	AG	1392		
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Qy	1393	AG	AG	CT	CT	TC	GA	AG	CT	AG	AG	CC	CA	AA	CC	GT	TAT	AT	CA	TAT	CT	AT	CT	AT	CT	CA	AG	NA	1452	
Db	1156	AG	AG	CA	CC	CT	GC	AA	TG	CA	CC	AG	AG	CC	TC	AG	AG	CA	GT	TAT	CAT	TG	TAT	GT	AT	GA	GA	NA	1215	
Qy	1453	AG	GG	GA	GT	TT	GA	AT	GG	AT	TC	CA	AT	TT	AC	CT	GA	GG	CT	TA	AG	CA	AA	TT	TA	ACT	CT	GA	AT	1512
Db	1216	AG	AG	CA	CG	TT	GA	AT	GG	AA	TCC	AT	CT	TT	CT	GA	AG	GA	TG	GA	AA	CT	GA	CT	CT	CT	GA	AG	CT	1275
Qy	1513	GT	CA	AG	CG	CT	GT	TT	TT	GA	AG	TT	CA	CT	CC	CT	GA	AT	CT	CT	GC	CT	CT	CT	CT	CT	GA	AG	ACT	1572
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Qy	1573	GA	AA	GC	CT	GA	AG	TT	TA	AG	AG	GG	GG	AG	TG	CT	TT	AA	AA	CT	CT	CA	AA	AT	TA	TAC	CC	AA	TT	1632
Db	1336	GA	AA	AC	CC	CG	GA	GT	TT	AA	AG	AG	AG	AG	CG	GA	AG	CT	TT	AG	AG	TAG	AT	TAT	CT	AT	CT	AT	TT	1395
Qy	1633	GG	CT	TG	AC	AC	AG	AC	AG	CT	CT	TT	TAT	AC	CT	TC	AG	CT	TC	AA	AG	GG	TG	AT	CT	GA	TT	TC	AG	1692
Db	1396	GG	TC	GACT	CA	AA	GA	CA	AG	CT	CT	TT	TACA	AA	CT	TT	CA	AA	TT	TC	GA	AG	GA	AA	TT	CA	AG	TC	AG	1455
Qy	1693	AG	TC	ACT	TC	GG	GA	AA	CA	CT	CT	TG	TG	CC	AA	GT	TT	CA	AG	TC	AT	TT	TC	GT	TA	1742				
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ATH345084																														
LOCUS																														
ATH345084 1729 bp mRNA linear PLN 20-SEP-2001																														

RESULT 4
ATH345084

31

Db	1216	TGGAATACGAGGGTCTTCAGATTCTTTCAAGGCACCTTGTGTGATATGGCTGCTGTACAC	1275
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Qy	1381	CCAAGCCTTAAGACAGCTCTTCGCAAGT--GCACAGAGGGCCAGAACCCCTATATCCT	1437
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Qy	1438	ATCTATGTCAGAGAAAGGGAGGTTTGAGATGGAGTCCATTTACTCTGAGGTCTAGCAAT	1497
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Db	1456	GTCACTCAGGAAGCTCTAGAAATCTGCAGTCTCTGCCAAGTTCAAGTCTTTAAACATGAG	1515
Qy	1558	CTGTATGGAAGACTGAAAGCGCTGAAGTATATAGAGAGGGGAGTCTTTTAAACCTCTAC	1617
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ATH404861			
LOCUS			
DEFINITION			
Arabidopsis thaliana mRNA for truncated alpha1.3-fucosyltransferase (FucTB gene).			
ACCESSION			
AJ404861.2 GI:21912393			
VERSION			
alpha 1.3-fucosyltransferase; FucTB gene.			
KEYWORDS			
Arabidopsis thaliana			
SOURCE			
Arabidopsis thaliana			
ORGANISM			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE			
1 Wilson, I.B., Rendic, D., Freilinger, A., Dumlac, J., Altman, F., Mucha, J., Muller, S. and Hauser, M.T.			
Cloning and expression of cDNAs encoding alpha1.3-fucosyltransferase homologues from Arabidopsis thaliana			
Biochim. Biophys. Acta 1527 (1-2), 88-96 (2001)			
2 Wilson, I.B., Rendic, D., Freilinger, A., Dumlac, J., Altman, F., Mucha, J., Muller, S. and Hauser, M.T.			
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Biochim. Biophys. Acta 1527 (1-2), 88-96 (2001)			
TITLE			
Cloning and expression of cDNAs encoding alpha1.3-fucosyltransferase homologues from Arabidopsis thaliana			
JOURNAL			
Biochim. Biophys. Acta 1527 (1-2), 88-96 (2001)			
MEDLINE			
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REFERENCE			
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TITLE			
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JOURNAL			
Biochim. Biophys. Acta 1527 (1-2), 88-96 (2001)			
MEDLINE			
21313304			
REFERENCE			
2 Wilson, I.B., Rendic			

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 2232)
AUTHORS v Zina L.P. and D'Aoust, M.A.
TITLE Method for regulating transcription of foreign genes in the presence of nitrogen
JOURNAL Patent: WO 0125454-A 12 12-APR-2001;
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Sequences to be used as promoter for regulating expression of foreign genes"
BASE COUNT 686 a 436 c 362 g 748 t
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Best Local Similarity 66.5%; Pred. No. 2.8e-42;
Matches 341; Conservative 0; Mismatches 151; Indels 21; Gaps 2;
QY 1486 AGGCTAGCAATTTAACTCTGAATGCTGTGAAGGCTGCTGTTGTTGAAGTTTCACATCC 1545
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DB 530 ATGCGCTTGTATGCTAGCTTCTTGCCCAACTCATCGGGGATTTGATGTTT 589
QY 1885 GTATAAGACATCACACTTTAAATTTTAAACTTTTCTGTAGAGTGCAGAAATCCATATTTA 1944
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DB 650 ATGTTGGTTGTAGTCTTATGATCATCT 682
RESULT 15
AX105536
LOCUS 2808 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 2 from Patent WO0125454.
ACCESSION AX105536
VERSION AX105536.1 GI:13921580
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 2808)
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JOURNAL Patent: WO 0125454-A 2 12-APR-2001;
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/db_xref="taxon:32630"
/note="Sequences to be used as promoter for regulating expression of foreign genes"
BASE COUNT 879 a 502 c 481 g 946 t
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QY 1779 AGCTTCACTAGCTAGCACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 1838
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DB 1329 ATACATGACTTCAACCATACTTAAACCCCTTTTGTAGAGTGCAGAAATCCATATTTA 1944
QY 1945 ATGCTTAGTTTGTAGTCTTATGATCATCT 1977
DB 1389 ATGTTGGTTGTAGTCTTATGATCATCT 1421
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Job time : 5634 secs

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QY 1546 CTGAATCTTGTGCTGTATGAAGACTGAAGGCTGAAGTCTGAAGTTTAAGAGGGGAGTGC 1605
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QY 1885 GTATAAGACATCACACTTTAAATTTTAAACTTTTCTGTAGAGTGCAGAAATCCATATTTA 1944
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